

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 20, 2003, 10:40:37 ; Search time 259 Seconds
(without alignments)
6910.144 Million cell updates/sec

Title: US-09-909-207-1

Perfect score: 663

Sequence: 1 CAATGTCACGCAATTC.....TAACCTTGATATAAACAAAT 663

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_15Jun03.*

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24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
25: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	663	100.0	663	17 AAT16101	Xylanase gene. Ba
2	663	100.0	744	17 AAT16102	Xylanase precursor
3	663	100.0	1513	17 AAT16103	Xylanase gene. Ba
4	634.2	95.7	744	19 AAV13067	Glycosyl hydrolase
5	634.2	95.7	871	19 AAV30255	DNA encoding a Bac
6	624.6	94.2	744	15 AAV30255	Thermostable alkal
7	507.8	76.6	747	19 AAV13074	Xylanase activity
8	255.4	38.5	2364	21 AA251821	Clostridium sterco

9	255.2	38.5	1022	16 AAQ80923	B. pumilus xylanase
10	212.2	32.0	1190	18 AAT90972	Nucleotide sequenc
11	204.8	30.9	1244	17 AAT08142	Xylanase xynD gene
12	154.4	23.3	164	16 AAQ92876	Thermostable alkal
13	151.2	22.8	164	16 AAQ92875	Thermostable alkal
14	119.4	18.0	1375	17 AAX90405	Actinomadura sp. D
15	119.4	18.0	1375	18 AAT64930	Actinomadura flexu
16	119	17.9	229	19 AAV15063	Xylanase activity
17	118.4	17.9	573	19 AAV36098	DNA sequence of th
18	117.8	17.8	1207	17 AAT42374	Bacillus sp. therm
19	115.2	17.4	213	19 AAV15059	Xylanase activity
20	115.2	17.4	596	21 AAX48219	T. reesei xylanase
21	115.2	17.4	596	24 AAD29410	Trichoderma reesei
22	111.8	16.9	1273	16 AAQ90388	Xylanase xynA gene
23	108.2	16.3	801	22 AAI66600	Bacillus haloduran
24	106	16.0	2898	21 AA246404	Penicillium funicu
25	105.8	16.0	1195	20 AA228864	Streptomyces oliva
26	105.8	16.0	1195	20 AA228865	Streptomyces oliva
27	104.4	15.7	851	18 AAT63044	Aspergillus niger
28	103	15.5	1281	18 AAT71585	Chaetomium thermop
29	100.8	15.2	1581	15 AAQ69150	Aspergillus tubige
30	100.8	15.2	3105	21 AA251819	Ruminococcus xylan
31	100.4	15.1	234	19 AAV15064	Xylanase activity
32	100.4	15.1	807	18 AAT71749	Fibrobacter succin
33	100.4	15.1	3141	18 AAT71746	Fibrobacter succin
34	98.8	14.9	648	18 AAT71748	Fibrobacter succin
35	98	14.8	1027	22 AAF85591	Acrononium cellulo
36	93.4	14.1	675	14 AAQ36563	Endo-xylanase gene
37	92	13.9	164	16 AAQ92877	Thermostable alkal
38	91	13.7	1015	14 AAQ54775	T. reesei xln2 gen
39	91	13.7	1015	20 AAV81332	T. reesei xylanase
40	89.6	13.5	822	19 AAV29598	DNA sequence of th
41	88.2	13.3	234	19 AAV15056	Xylanase activity
42	87.2	13.2	941	14 AAQ54776	T. reesei xln1 gen
43	87.2	13.2	941	20 AAV81331	T. reesei xylanase
44	87.2	13.2	2338	15 AAQ54656	Plasmid pNX1 compr
45	87	13.1	234	19 AAV15058	Xylanase activity

ALIGNMENTS

RESULT 1

AAT16101
ID AAT16101 standard; DNA; 663 BP.

XX AAT16101;

DT 15-MAY-1996 (first entry)

XX Xylanase gene.

XX Xylanase; thermostable enzyme; paper; pulp; bleaching; feedstuff;
baking; ss.

OS Bacillus sp. strain 710/1 (LMG P-14798).

XX Key Location/Qualifiers

FT mat_peptide 1..663

FT /*tag= a

FT /EC_number= 3.2.1.8

XX AU9525086-A.

XX 08-FEB-1996.

XX 19-JUL-1995; 95AU-0025086.

XX 17-MAY-1995; 95BE-0000448.

XX 26-JUL-1994; 94BE-0000706.

XX (SOLV) SOLVAY SA.

PA (SOLV) SOLVAY & Cie.

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XX De Buyl E, Detroz R, Lahaye A, Ledoux P;
XX WPI; 1996-117341/13.
XX P-PSDB; AAR92053.
XX Bacillus derived xylanase active over wide pH range - used in
XX treatment of paper pulp, animal feeds and in bakery goods
XX
XX Claim 30; Page 50-51; 94pp; English.
XX
XX A DNA sequence (AAT16101) coding for a thermostable mature xylanase
XX (AAR92053) was isolated from a gene library of Bacillus sp. 720/1
XX (LMG P-14798). Sequences were also obtd. (see AAT16102 and AAT16103)
XX for the xylanase precursor and for the complete gene including 5'
XX and 3' untranslated sequences. DNA coding for the mature enzyme
XX may be incorporated into a vector and expressed from either its
XX own promoter or from the Bacillus pumilus PRL B12 promoter (AAQ73996),
XX and used for prodn. of recombinant xylanase in transformed hosts,
XX pref. Bacillus licheniformis or B. pumilus. The enzyme is useful
XX in the paper-pulp, animal feed and baking industries.
XX
SQ Sequence 663 BP; 220 A; 131 C; 146 G; 166 T; 0 other;

Query Match      100.0%; Score 663; DB 17; Length 663;
Best Local Similarity 100.0%; Pred. No. 1.3e-188;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAATCGTACCGACCAATTCATTTGGCAACGAGATGGCTATGATTAATTTGGAAA 60
DB 1 CAAATCGTACCGACCAATTCATTTGGCAACGAGATGGCTATGATTAATTTGGAAA 60
QY 61 GATAGCGGTGGCTCTGGGCAATGATTCATTCATGAGCGGTACGTTCCAGTCCCAATG 120
DB 61 GATAGCGGTGGCTCTGGGCAATGATTCATTCATGAGCGGTACGTTCCAGTCCCAATG 120
QY 121 AACATGTTAACACATATTTATTCCTTAAGGTAATAATTCATTAACACAAACACAC 180
DB 121 AACATGTTAACACATATTTATTCCTTAAGGTAATAATTCATTAACACAAACACAC 180
QY 181 CAACAAGTGTGAACATGTCATTAACCTACGAGACCACTCCCAACCAATGGTATGCG 240
DB 181 CAACAAGTGTGAACATGTCATTAACCTACGAGACCACTCCCAACCAATGGTATGCG 240
QY 241 TATTTATGCGTCTATGCTGAGCTGTGACCTCTTTCGCAATTAATTTGTCGACGT 300
DB 241 TATTTATGCGTCTATGCTGAGCTGTGACCTCTTTCGCAATTAATTTGTCGACGT 300
QY 301 TGGGCGCACTGGCTCCACGAGAGACGCTTAAGGGGACATCACTGTTGATGAGGA 360
DB 301 TGGGCGCACTGGCTCCACGAGAGACGCTTAAGGGGACATCACTGTTGATGAGGA 360
QY 361 ACATATGATATCTACGAGACTCTTAAGATCAATCAACCTCCATTAAAGGGATGCGACA 420
DB 361 ACATATGATATCTACGAGACTCTTAAGATCAATCAACCTCCATTAAAGGGATGCGACA 420
QY 421 TTTAAACAATATTGAGGTTCGAAAGATCGAAACGACGAGTGGCGCATTTCTGTACG 480
DB 421 TTTAAACAATATTGAGGTTCGAAAGATCGAAACGACGAGTGGCGCATTTCTGTACG 480
QY 481 AACCACTTAAAGCGTGGGAAAACTTAAGGATCAATTAAGGGGAAAAATGTAAGTCGG 540
DB 481 AACCACTTAAAGCGTGGGAAAACTTAAGGATCAATTAAGGGGAAAAATGTAAGTCGG 540
QY 541 CTTACTGTGAAGGCTATCAAAAGTAGCGGAAGTCTAATGTATATGCAATACACTAAGA 600
DB 541 CTTACTGTGAAGGCTATCAAAAGTAGCGGAAGTCTAATGTATATGCAATACACTAAGA 600
QY 601 ATTTAAGGTACCCCTCTCTCAACTATTAATGACGAGACATACTTTGATATAAAC 660
DB 601 ATTTAAGGTACCCCTCTCTCAACTATTAATGACGAGACATACTTTGATATAAAC 660
QY 661 AAT 663

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DB 661 AAT 663
|||
RESULT 2
ID AAT16102 standard; DNA; 744 BP.
AC AAT16102;
DE 15-MAY-1996 (first entry)
XX Xylanase precursor gene.
XX Xylanase; thermostable enzyme; paper; pulp; bleaching; feedstuff;
XX baking; ss.
XX
XX Bacillus sp. strain 710/1 (LMG P-14798).
XX
XX Key Location/Qualifiers
FH sig_peptide 1..81
FT /tag= a
FT mat_peptide 82..744
FT /tag= b
FT /EC_number= 3.2.1.8
XX
XX AU9525086-A.
XX
XX 08-FEB-1996.
XX
XX 19-JUL-1995; 95AU-0025086.
XX
XX 17-MAY-1995; 95BE-0000448.
XX 26-JUL-1994; 94BE-0000706.
XX
XX (SOLV ) SOLVAY SA.
XX (SOLV ) SOLVAY & CIE.
XX
XX De Buyl E, Detroz R, Lahaye A, Ledoux P;
XX WPI; 1996-117341/13.
XX P-PSDB; AAR92054.
XX
XX Bacillus derived xylanase active over wide pH range - used in
XX treatment of paper pulp, animal feeds and in bakery goods
XX
XX Claim 9; Page 54-55; 94pp; English.
XX
XX A DNA sequence (AAT16102) coding for a xylanase precursor (AAR92054)
XX was isolated from a gene library of Bacillus sp. 720/1 (LMG P-14798).
XX The sequence (AAT16103) for the complete gene including 5' and 3'
XX untranslated sequences was also obtd. The gene may be incorporated
XX into a vector and expressed from either its own promoter or from the
XX Bacillus pumilus PRL B12 promoter (see AAQ73996), and used for prodn. of
XX recombinant thermostable xylanase in transformed hosts, pref. Bacillus
XX licheniformis or B. pumilus. The enzyme is useful in the paper-pulp,
XX animal feed and baking industries.
XX
SQ Sequence 744 BP; 246 A; 144 C; 160 G; 194 T; 0 other;

Query Match      100.0%; Score 663; DB 17; Length 744;
Best Local Similarity 100.0%; Pred. No. 1.4e-188;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAATCGTACCGACCAATTCATTTGGCAACGAGATGGCTATGATTAATTTGGAAA 60
DB 82 CAAATCGTACCGACCAATTCATTTGGCAACGAGATGGCTATGATTAATTTGGAAA 141
QY 61 GATAGCGGTGGCTCTGGGCAATGATTCATTCATGAGCGGTACGTTCCAGTCCCAATG 120
DB 142 GATAGCGGTGGCTCTGGGCAATGATTCATTCATGAGCGGTACGTTCCAGTCCCAATG 201
QY 121 AACATGTTAACACATATTTATTCCTTAAGGTAATAATTCATTAACACAAACACAC 180

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XX PA (NOVO ) NOVO-NORDISK AS.
XX PI Outtrup H, Biegard-frantzen H, Schuelein M, Olsen AA, Jorgensen PL,
XX PI Dambmann C;
XX DR WPI; 1998-376805/32.
XX DR P-PSDB; AAW60562.
XX
XX PT DNA construct encoding Bacillus agaradherens xylanolytic enzyme -
XX PT and vectors and Bacillus cells containing these, useful for
XX PT recombinant production of the enzyme for use in agricultural waste
XX PT breakdown and lignocellulosic material treatment
XX
XX PS Claim 1; Columns 11-14; 10pp; English.
XX
XX CC The present sequence encodes a xylanolytic enzyme of Bacillus
XX CC agaradherens NCIMB 40482. Xylanolytic enzymes are used for enzymatic
XX CC breakdown of agricultural wastes for production of alcohol fuels,
XX CC enzymatic treatment of animal feeds to release free pentose sugars,
XX CC manufacturing of dissolving pulps yielding cellulose and bio-bleaching
XX CC of wood pulp. They are also used for treatment of lignocellulosic
XX CC material e.g. paper and pulp, or as an animal feed additive.
XX CC (Updated on 25-MAR-2003 to correct PR field.)
XX CC (Updated on 25-MAR-2003 to correct PI field.)
XX
XX SQ Sequence 871 BP; 283 A; 171 C; 179 G; 238 T; 0 other;
Query Match 95.7%; Score 634.2; DB 19; Length 871;
Best Local Similarity 97.3%; Pred. No. 6.5e-180;
Matches 645; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
QY 1 CAATCGTCACCGACAATTCCATTGGCAACACGATGGCTATGATTATGAATTTGGAAA 60
DB 82 CAATCGTCACCGACAATTCCATTGGCAACACGATGGCTATGATTATGAATTTGGAAA 141
QY 61 GATAGCGGTGGCTCTGGGACAATGATTTCTCAATCATGGCGGTACGTTCAAGTCCCAATGG 120
DB 142 GATAGCGGTGGCTCTGGGACAATGATTTCTCAATCATGGCGGTACGTTCAAGTCCCAATGG 201
QY 121 AACATGTTTAAACAATATTATTCGGTAAAGTAAATAAATTCATGAACACACACAC 180
DB 202 AACATGTTTAAACAATATTATTCGGTAAAGTAAATAAATTCATGAACACACACAC 261
QY 181 CAACAAGTTGTAACATGTCCTCAATAAATACGAGGCAATCTTCCAAACCAATGGTAATCGG 240
DB 262 CAACAAGTTGTAACATGTCCTCAATAAATACGAGGCAATCTTCCAAACCAATGGTAATCGG 321
QY 241 TATTATGCGTCTATGTTGGACTGTTGACCCCTCTTGTGCGAATATTAATTTGTCGACAGT 300
DB 322 TATTATGCGTCTATGTTGGACTGTTGACCCCTCTTGTGCGAATATTAATTTGTCGATAGT 381
QY 301 TGGGCACTGGCGTCCACGAGGACGACGCTTAAGGGGACCATCTGTTGATGGAGGA 360
DB 382 TGGGCACTGGCGTCCACGAGGACGACGCTTAAGGGGACCATCTGTTGATGGAGGA 441
QY 361 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCTCCATTAAAGGATTTGCCACA 420
DB 442 ACATATGATATCTAGAACTCTTAGAGTCAATCAACCTCCATTAAAGGATTTGCCACA 501
QY 421 TTTAAACAATATTTGAGTGTTCGAAGATCGAAACCGCAGAGTGGCAGATTTCTGTACG 480
DB 502 TTTAAACAATATTTGAGTGTTCGAAGATCGAAACCGCAGAGTGGCAGATTTCTGTACG 561
QY 481 AACCACTTTAGAGCGTGGGAAACTTTAGGATGATATATGGGAAATCTATGAAGTCCGG 540
DB 562 AACCACTTTAGAGCGTGGGAAACTTTAGGATGATATATGGGAAATCTATGAAGTCCGG 621
QY 541 CTTACTGTAGAGGCTATCAAGTAGCGGAAGTGTCTAATGTATATAGCAATACACTAAGA 600
DB 622 CTTACTGTAGAGGCTATCAAGTAGCGGAAGTGTCTAATGTATATAGCAATACACTAAGA 681
QY 601 ATTAACGGTAACCCCTCTCTCAACTATTAGTAATAGCAGAGACATAAATTTGGATAAAAAC 660
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DB 682 ATTAACGGTAACCCCTCTCTCAACTATTAGTAATGACAAGACATAAATCTAGATAAAAAC 741
QY 661 AAT 663
DB 742 AAT 744
RESULT 6
AAQ92878
ID AAQ92878 standard; DNA; 744 BP.
XX AC AAQ92878;
XX
XX DT 12-FEB-1996 (first entry)
XX
XX DE Thermostable alkaline endo-1,4-beta-D-xylanase gene.
XX
XX KW thermostable alkaline endo-1,4-beta-D-xylanase gene; cloning;
XX KW polymerase chain reaction; Escherichia coli; EC-3.2.1.8; paper;
XX KW pulp; bleaching; ds.
XX
XX OS Bacillus sp. 1-43-3 (CBS 672.93).
XX
XX PN WO9518219-A1.
XX
XX PD 06-JUL-1995.
XX
XX PF 23-DEC-1994; 94WO-EP04312.
XX
XX PR 24-DEC-1993; 93EP-0203694.
XX
XX PA (KONN ) GIST-BROCADES NV.
XX
XX PI Farrell RL, Goedegebuur F, Herbes WT, Herweijer MA;
XX PI Iverson S, Jones BE, Quax WJ, Van Beckhoven RFWC;
XX PI Van der Kleij WA, Van Solingen P, Williams DP;
XX
XX DR WPI; 1995-246385/32.
XX
XX P-PSDB; AAR76551.
XX
XX Novel xylanase enzyme active at high pH - useful in paper and pulp
XX prodn. processes
XX
XX Claim 4; Page 42-43; 54pp; English.
XX
XX The sequence encodes an alkaline endo-1,4-beta-D-xylanase (G-type)
XX from Bacillus sp. 1-43-3. Fragments of the sequence (e.g. the
XX internal fragments given in AAQ92876 and AAQ92877) may be amplified
XX by polymerase chain reaction, e.g. using primers with sequences
XX AAQ92866, AAQ92867, AAQ92868 and AAQ92869. The DNA may be cloned in
XX Escherichia coli using a plasmid vector for recombinant xylanase
XX production. The xylanase may be used in the paper and pulp
XX industries, where it produces an increase in % ISO brightness of
XX softwood pulp of at least 1.0 over non-enzymatically treated pulp
XX in an ECF pulp bleaching process, at pH 9.0 and 65 deg C. The
XX enzyme may be used in production of paper, board and fluff pulp,
XX and has low cellulase activity. The increased brightness
XX produced using the xylanase allows reduction in the amount of
XX bleaching chemicals used.
XX
XX SQ Sequence 744 BP; 248 A; 145 C; 159 G; 192 T; 0 other;
Query Match 94.2%; Score 624.6; DB 16; Length 744;
Best Local Similarity 96.4%; Pred. No. 4.6e-177;
Matches 639; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 1 CAATCGTCACCGACAATTTCCATTGGCAACCAACCATGGCTATGATTATGAATTTGGAAA 60
DB 79 CAATCGTCACCGACAATTTCCATTGGCAACCGCGGTGTTATGATTATGAATTTGGAAA 138
QY 61 GATAGCGGTGGCTCTGGGACAATGATTTCTCAATCATGGCGGTACGTTCAAGTCCCAATGG 120
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Db      139 GATACGGGTGGCTGGGACATGATTCATTCATGGGGTACGTTCCCAATGG 198
Qy      121 AACATGTTAACACATATTTATTCGTAAAGTTAAATAATGAAACACAAACACAC 180
Db      199 AATAATGTTAACATATATTTATTCGTAAAGTTAAATAATGAAACACAAACACAC 258
Qy      181 CAACAAGTTGGTACATGTCCTAAACTACGAGCCAACTTCCAAACCAATGGTATGG 240
Db      259 CAACAAGTTGGTACATGTCCTAAACTACGAGCCAACTTCCAAACCAATGGTATGG 318
Qy      241 TATTTATGCGTCTATGATGTTGACGTTGACCTCTTGTGCAATATATATTTGCAAGT 300
Db      319 TATTTATGCGTCTATGATGTTGACGTTGACCTCTTGTGCAATATATATTTGCAAGT 378
Qy      301 TGGGGCAACTGGCGTCCACACAGAGCAACGCTTAAGGGGACATCACTGTTATGAGGA 360
Db      379 TGGGGCAACTGGCGTCCACACAGAGCAACGCTTAAGGGGACATCACTGTTATGAGGA 438
Qy      361 ACATATGATATCTACAGACTCTTACAGTCATCAACCTTCCATTAAGGGGATGGCCACA 420
Db      439 ACATATGATATCTACAGACTCTTACAGTCATCAACCTTCCATTAAGGGGATGGCCACA 498
Qy      421 TTTAAACAATATTTGAGTGTGAGATGAGAAACGACAGAGTGGCAGATTTCTGTACG 480
Db      499 TTTAAACAATATTTGAGTGTGAGATGAGAAACGACAGAGTGGCAGATTTCTGTACG 558
Qy      481 AACCACTTTAGACGCTGGGAAAACTTAGGATGATATATGAGGAAAAATGATGAGTGGC 540
Db      559 AACCACTTTAGACGCTGGGAAAACTTAGGATGATATATGAGGAAAAATGATGAGTGGC 618
Qy      541 CTTACTGTGAGAGGCTATCAAAAGTAGCCGAAAGTCTTAATGATATGCAATACATCAAA 600
Db      619 CTTACTGTGAGAGGCTATCAAAAGTAGCCGAAAGTCTTAATGATATGCAATACATCAAA 678
Qy      601 ATTAACGGTAACCCCTCTCAACTATTAATGATGAGAGCAATACCTTGGATTAATAAC 660
Db      679 ATTAACGGTAACCCCTCTCAACTATTAATGATGAGAGCAATACCTTGGATTAATAAC 738
Qy      661 AAT 663
Db      739 AAT 741

RESULT 7
AAV13074
ID      AAV13074 standard; DNA; 747 BP.
XX      AAV13074;
XX      19-MAY-1998 (first entry)
XX      Xylanase activity positive clone DNA SEQ ID NO:11.
XX      Bacillus sp.; xylanase; glycosyl hydrolase family 11; isolation;
XX      microorganism; identification; hybrid DNA; ss.
XX      Synthetic.
XX      Bacillus sp.
XX      Key      Location/Qualifiers
XX      CDS      1..747
XX      FT      /tag= a
XX      /product= "positive clone for xylanase activity"
XX      MO9743409-A2.
XX      20-NOV-1997.
XX      12-MAY-1997; 97WO-DK00216.
XX      10-MAY-1996; 96DK-0000562.
XX      (NOVO ) NOVO-NORDISK AS.
PA

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XX      Dalboge H, Diderichsen B, Kauppinen S, Sandel T;
XX      WPI; 1998-008878/01.
XX      Isolating novel DNA sequences from microorganisms - without the need
XX      for culturing the microorganism
XX      Example 1; Page 35; 72pp; English.
XX      The present sequence represents a positive clone for xylanase activity
XX      from an example of the present invention. The present invention
XX      describes a novel method for providing a novel DNA sequence encoding a
XX      polypeptide from a microorganism with an activity of interest. The
XX      method comprises: (i) PCR amplification of the DNA with PCR primers with
XX      homology to (a) known gene(s) encoding a polypeptide with an activity of
XX      interest; (ii) linking the obtained PCR product of a 5' structural gene
XX      sequence and a 3' structural gene sequence; (iii) expressing the
XX      resulting hybrid DNA sequence; (iv) screening for hybrid DNA sequences
XX      encoding a polypeptide with the activity of interest or a related
XX      activity; and (v) isolating the hybrid DNA sequence identified in step
XX      (iv). This method provides for identification and isolation of sequences
XX      from microorganisms without having to cultivate and isolate the
XX      microorganism.
XX      Sequence 747 BP; 236 A; 168 C; 154 G; 189 T; 0 other;
XX      Query Match      76.6%; Score 507.8; DB 19; Length 747;
XX      Best Local Similarity 85.4%; Pred. No. 5e-142;
XX      Matches 566; Conservative 0; Mismatches 97; Indels 0; Gaps 0;
Qy      1 CAATCGTCCAGCAATATTCATTTGGCAACCAAGTGGCTATGATTAATTTTGGAAA 60
Db      82 CAATCGTCCAGCAATATTCATTTGGCAACCAAGTGGCTATGATTAATTTTGGAAA 141
Qy      61 GATACGGGTGGCTGGGACATGATTTCTCATATGAGCGGTAAGTTCAGTGGCCAAATGG 120
Db      142 GATACGGGTGGCTGGGACATGATTTCTCATATGAGCGGTAAGTTCAGTGGCCAAATGG 201
Qy      121 AACATGTTAACACATATTTATTCGTAAGGTAAATAATTCATGAAACACAAACACAC 180
Db      202 AACATGTTAACACATATTTATTCGTAAGGTAAATAATTCATGAAACACAAACACAC 261
Qy      181 CAACAAGTTGGTACATGTCCTAACTAACTAGGAGCAACTTCCAAACCAATGTTATGCG 240
Db      262 CAACAAGTTGGTACATGTCCTAACTAACTAGGAGCAACTTCCAAACCAATGTTATGCG 321
Qy      241 TATTTATGCGTCTATGATGTTGACCTCTTGTGCAATATATATTTGTCAGCAGT 300
Db      322 TATTTATGCGTCTATGATGTTGACCTCTTGTGCAATATATATTTGTCAGTAGT 381
Qy      301 TGGGGCAACTGGCGTCCACACAGAGCAACGCTTAAGGGGACATCACTGTTATGAGGA 360
Db      382 TGGGGCAACTGGCGTCCACACAGAGCAACGCTTAAGGGGACATCACTGTTATGAGGA 441
Qy      361 ACATATGATATCTACAGACTCTTACAGTCATCAACCTTCCATTAAGGGGATGGCCACA 420
Db      442 ACATATGATATCTACAGACTCTTACAGTCATCAACCTTCCATTAAGGGGATGGCCACC 501
Qy      421 TTTAAACAATATTTGAGTGTGAGATGAGAAACGACAGATGGGACGATTTGTCAGC 480
Db      502 TTTCAATGATATCTGATGTCATTCGACAGACGAGCAACGCGGACATCTGATCAACGGA 561
Qy      481 AACCACTTTAGACGCTGGGAAAACTTAGGATGATATGAGGAAAAATGATGAACTGCG 540
Db      562 AACCACTTTAGACGCTGGGAAAACTTAGGATGATATGAGGAAAAATGATGAACTGCG 621
Qy      541 CTTACTGTGAGAGGCTATCAAAAGTAGCCGAAAGTCTATATGATGCAATACATAAGA 600
Db      622 CTTACTGTGAGAGGCTATCAAAAGTAGCCGAAAGTCTATATGATGCAATACATAAGA 681
Qy      601 ATTAACGGTAACCCCTCTCAACTATTAATGATGAGAGCAATACCTTGGATTAATAAC 660

```

Db 682 ATTAACGGTAACCTCTCTCAACTATTAGTAATGACAAGAGCATAACTCTAGATAAAAAAC 741

Qy 661 AAT 663

Db 742 AAT 744

RESULT 8

AAZ51821

ID AAZ51821 standard; DNA; 2364 BP.

XX.

AC AAZ51821;

XX

DT 04-JUL-2000 (first entry)

XX

DE Clostridium stercorarium xylanase A DNA.

XX

KW Xylanase A; XynA; cellulosome; feruloyl esterase; phenolic acid esterase;

KW thermostable; ferulic acid; wheat bran; agricultural byproduct; treat;

KW grass; paper and pulp industry; feed processing; food additive;

KW plant cell wall material; degradation; ds.

XX

OS Clostridium stercorarium.

XX

FH Key Location/Qualifiers

FT CDS 440..1978

FT /tag= e

FT /product= "Xylanase A"

XX

PN WO200014243-A1.

XX

PD 16-MAR-2000.

XX

PF 03-SEP-1999; 99WO-US20304.

XX

PR 04-SEP-1998; 98US-0099136.

XX

PA (UTGE-) UNIV GEORGIA RES FOUND INC.

XX

PI Blum DL, Kataeva I, Li X, Ljungdahl LG;

XX

DR WPI; 2000-256991/22.

XX

DR P-P8DB; AAY70523.

XX

PT New recombinant DNA molecule comprising a sequence encoding feruloyl

PT esterase protein, useful for treating grasses and other plant materials

PT used in pulp and paper industries, feed processing and food additives -

XX

PS Disclosure; Pages 97-99; 105pp; English.

XX

CC The present sequence is a DNA encoding xylanase A (XynA) from

CC Clostridium stercorarium. XynA contains family VI cellulose

CC binding domain (CBD) which is homologous to the CBD of xylanase Z

CC (XynZ) of Clostridium thermocellum. XynZ is an enzymatic component of

CC C. thermocellum cellulosome and has a multi-domain structure which

CC includes a dockerin domain, a catalytic xylanase domain,

CC a family VI cellulose binding domain and a domain of

CC unknown function. The unknown domain in the N-terminal region of XynZ

CC has been found to contain feruloyl (phenolic acid) esterase which

CC is involved in the degradation of plant cell wall material. The novel

CC feruloyl esterase is thermostable, easy to purify, has high temperature

CC optima and stable over a wide pH range. The enzyme is used for

CC producing ferulic acid from wheat bran or agricultural byproducts,

CC treating grasses or other plant materials used in the pulp and paper

CC industries, in feed processing and as a food additive.

XX

SQ Sequence 2364 BP; 791 A; 428 C; 458 G; 587 T; 0 other;

XX

Query Match 38.5%; Score 255.4; DB 21; Length 2364;

Best Local Similarity 65.6%; Pred. No. 4.2e-66;

Matches 405; Conservative 0; Mismatches 206; Indels 6; Gaps 2;

Qy

1 CAATCGTCACCGACAATTCATTTGGCAACCAACGATGGCTATGATTAATTTGGAAA 60

Db	533	CGAATAATTTACGACAAATGAGACAGGCACACATCGAGGCTACGACTATGAGCTCTGGAAA	592
Qy	61	GATAGCGGTGGCTCTGGGACAAATGATTCTCAATCATGGCGGTACGTTCCAGTGCCTCAATGG	120
Db	593	GA---CTACGGGAATACGATTATGGAATTAACGACGGTGGTACTTTTAGTTGTCAATGG	649
Qy	121	AACAATGTTAAACAACATATTATTCGTAAGGTAAAAAATTCATTAAGAAACAACAACACAC	180
Db	650	AGTAATATCGGTAATGCACATATTTAGAAAAGGGAGAAAATTTAATTCGACACAACCTAT	709
Qy	181	CAACAAGTTGTAACATGTCCATAAATACGAGGACCACTTCCAAACCAAAATGGTATGG	240
Db	710	CAAGAATTTAGGAGACATAGTAGTTGAATATATGCTGTGTGATTACAATCCAAACCGAAATTC	769
Qy	241	TATTTATCGCTCTATGTTGGACTGTTGACCCCTCTTGTGCAATATTATTATTCGACAGT	300
Db	770	TATTTGTGTTTACGGTTGGACAAGAAATCCACTGTTGTAATATTACATTTGTAGAAAGC	829
Qy	301	TGGGGCAACTCGGCTCCACAGGAGCAACGCTTAAGGGGACCATCAC---TGTGTATGGA	357
Db	830	TGGGGCAGCTGGCGTCCACCTGGAGCAACACCCCAAGGAACCATCACACAGTGGATGGCA	889
Qy	358	GGACATATGATATCTACGAGACTTTAGAGTCAATCAACCCCTCAATTAAAGGGATTGCC	417
Db	890	GGTACTTATGAAATATATGAAACTACCGGGTAAATCAGCCTTCATCGATGGAACTCGG	949
Qy	418	ACATTTAAACAATATTGGAGTGTTCGAAGATCGAAACGACAGAGTGGGACCAAGTTCTGTC	477
Db	950	ACATTTCCACAATATTGGAGTGTTCGATACATCCAAGAGAACACGGGAACAATATCTGTC	1009
Qy	478	AGCAACCACTTTAGAGCGTGGGAAAACCTTAGGGATGAATATGGGAAAATGTATGAAGTC	537
Db	1010	ACTGAACATTTTAAACAGTGGGAAAGAAATGGGCATCGAATGGGTAAAGATGTATGAAGTT	1069
Qy	538	CGGCTTACTGTAGAGGCTATCAAGTAGCGGAAGTGTATGTATATAGCAATACACTA	597
Db	1070	GCTCTTACCGTTGAAGGTTATCAGAGCAGTGGGTACGCTAATGTATACAGAATAATC	1129
Qy	598	AGAAATTAACGGTAACCC 614	
Db	1130	AGAAATAGTGCAAAATCC 1146	
RESULT 9			
AAQ80923			
ID	AAQ80923	standard; DNA; 1022 BP.	
XX	AC	AAQ80923;	
XX	DT	02-AUG-1995 (first entry)	
XX	DE	B. pumilus xylanase gene.	
XX	KW	Xylanase; endo-1,4-beta-D-xylanase; wood pulp; pulping;	
XX	KW	biobleaching; bleaching; Bacillus licheniformis; ss.	
XX	OS	Bacillus pumilus.	
XX	FH	Key Location/Qualifiers	
FT	5'UTR	1..185	
FT		/tag= a	
FT		/note= "Claim 12"	
FT	misc_difference	107	
FT		/tag= b	
FT		/note= "base n at position 107 is not identified in the specification"	
FT	CDS	186..869	
FT		/tag= c	
FT	sig_peptide	186..266	
FT		/tag= d	
FT		/note= "Claim 11"	
FT	mat_peptide	267..866	

Best Local Similarity 62.4%; Pred. No. 2.9e-53;		Matches 369; Conservative 0; Mismatches 213; Indels 9; Gaps 2;	
Qy	3 AATCGTCACGACAAATTCATTTGGCAACACGATGGCTATGATTAATTTTGGAAAGA 62		
Db	150 AACACTACAGTAATGCAAGCGGTACTTTTGTATGGCTACTACTATGAACTATGGAAAGA 209		
Qy	63 TAGCGGTGGCTCTGGGCAATGATTTCTCAATCATGCGCGTACGTTCACTGCCCAATGAA 122		
Db	210 TA---CAGGGAATACACCATGCTGTATACACACAGGAAGGTTTGTCTGTAGTGGAG 266		
Qy	123 CAATGTTAAACACATATTATTCCTGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAG 182		
Db	267 CAATATAAACATGCAATTAATTCAGAACAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAG 320		
Qy	183 ACAAGTTGGTAACATGTCATATAAATCTAGCGAGCCAACTTCCAAACCAAAATGGTAATGCGTA 242		
Db	321 GTCATTAGGCACTATTAGNAATCACCTACTCAGCCACATATAATCTTAATGTTACTCTTA 380		
Qy	243 TTTATGCGCTATAGGTTGGAGCTGTTTGACCTCTTGTGCAATATTAATATTGTCGACAGTTG 302		
Db	381 CTTATGTATCTATGTTGGTCTCTACTTAATCTCTTTAGTAGAGTTTACATTTGTAGAAAGTTG 440		
Qy	303 GGGCAACTGGCGTCCACGAGGCAACCGCTTAAGGGGACCATCACTGTTGATGGAGAAC 362		
Db	441 GGGTAATTTGGCGTCCACGAGTGCACCTCTCTTGGACAGGTTACTATCGACGGTGTAC 500		
Qy	363 ATATGATATCTACGAGACTCTTAGAGTCAATCAACCTCCATTAAAGGGGATGGCCACATTT 422		
Db	501 CTAAGACATTTACAGAACTACCGGTGTAATCAGCCATCTATTGTCGGTACAGCTACTTT 560		
Qy	423 TAAACAATTTGGAGTGTTCGAAGATCGAAACGACAGTGGCAGCATTTCTGTGAGCAA 482		
Db	561 TGATCAATTTGGAGTGTAAAGACATCTAAGAGAACAAAGTGGAAACAGTCACTGTAACAGA 620		
Qy	483 CCACCTTAGAGGTTGGGAAACTTAGGATGAATATGGGAAATGTAATGAGTGGCGCT 542		
Db	621 TCACCTTAGGCGATGGGCAAAATAGAGGTTTAAACCTTGGTACTATTGATCAAAATTAATCT 680		
Qy	543 TACTGTAGAAGGCTATCAAGTAGCGGAAGTGCTAATGTATATAGCAATAC 593		
Db	681 TTGTGTTGAAGGATATCAAGCAGTGGTTGCGCTAATATACACAAATATAC 731		
RESULT 11			
ID	AAT08142		
XX	AAT08142 standard; DNA; 1244 BP.		
AC	AAT08142;		
XX	25-MAR-2003 (updated)		
DT	12-MAY-1996 (first entry)		
XX	Xylanase xynD gene.		
DE	Xylanase D; xynD gene; thermostable enzyme; paper; pulp; lignin;		
KW	delignification; xylan; bleaching; ds.		
XX	Extremophile isolate TG456 (CBS 213.94).		
OS	Key Location/Qualifiers		
FX	CDS 1..1107		
FT	/*tag= a		
XX	W09534662-A1.		
PN	21-DEC-1995.		
XX	14-JUN-1995; 95WO-EP02299.		
XX	14-JUN-1994; 94EP-0201699.		
PR	(KONN) GIST-BROCADES BV.		
FA			

XX

PI

Groenberg V, Williams DP, Iverson S, Forster S, Moody D;

PI

Farrel RL, Bergquist PL, Daniel RM, Morgan HW, Quax WJ;

XX

Herweijer MA, Jones BS;

DR

WPI; 1996-049690/05.

XX

P-PSDB; AAR87012.

XX

Novel xylanase(s) having activity at 80 deg.C or higher - obtained

PT

from anaerobic thermophilic bacteria and used in paper and pulp

PT

production processes

XX

Example 9; Page 56-58; 77pp; English.

PS

A full-length xynD gene (AAT08142) codes for a thermostable G-type

CC

xylanase (AAR87012) useful in the pulp and paper industries. The

CC

gene was obt'd. by genomic walking PCR of DNA from an extremely

CC

thermophilic bacterium, strain TG456 (CBS 213.94), isolated from a

CC

New Zealand hot spring. The gene can be inserted into a vector and

CC

used for the prodn. of recombinant xylanase D in microbial host

CC

cells, esp. Escherichia coli.

CC

(Updated on 25-MAR-2003 to correct PI field.)

XX

Sequence 1244 BP; 380 A; 215 C; 279 G; 360 T; 10 other;

SQ

Query Match 30.9%; Score 204.8; DB 17; Length 1244;

Best Local Similarity 61.0%; Pred. No. 4.8e-51;

Matches 367; Conservative 2; Mismatches 224; Indels 9; Gaps 2;

Qy

8 TCACCGCAATTCATTTGGCAACCCAGATGGCTATGATTAATTTTGGAAAGATGCG 67

Db

71 TTACCTCTAATGCAACTGGGACATACGATGTTTACTACGAGTTGTTGGGAAGACACAG 130

Qy

68 GTGCTCTGGGACAAATGATTTCTCAATCATGCGGTACGTTTCAGTGCCCAATGGGAACATG 127

Db

131 GGAATACT---ACCATGACAGTTGACACAGAGGAGATTTAGTGTGCTGGAGTAACA 187

Qy

128 TTAACAACATATTTATTCGTAAGGTAAAGGTAAAGGTAAAGGTAAAGGTAAAGGTAAAG 187

Db

188 TTAACAATGCACTCTTCAGAACAGTAAAGTTTATGACCTGTCATGGAATCAGC----- 241

Qy

188 TTGTTAATCATGTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 247

Db

242 TTGGGACTGTAAAGATTTACCTACTCTGCTACTACAAATCCAAATCCAAATCCAAATCC 301

Qy

248 GCGTCTATGTTGGACTGTTGACCCCTCTGTCGAATATTAATTAATTAATTAATTAATTAAT 307

Db

302 GCATTTATGATGTCGAAGAAATCCACTTTGTTGAATTTTATATCGTTGAAAGCTGGGGCT 361

Qy

308 ACTGGCGTCCACGAGGACCAACGCTTAAGGGGACCATCACTGTTGATGGAGGAAACATATG 367

Db

362 CATGGCGTCCCGCGGCAACGCTCACTTGGCACTGTAAACAATTTGATGGAGCAACATATG 421

Qy

368 ATATCTACGAGACTCTTTAGAGTCAATCAACCTTCATTAAGGGGATTTGCCACATTTAAAC 427

Db

422 ATATTTAAGACAACTCGTGTAAATCAGCCATCTATCGAAGGAAACAAAGAACTTTGATC 481

Qy

428 AATATTCGAGTGTTCGAAGATCGAAACGACGAGTGGCAAGATTTCTGTGACGACCACT 487

Db

482 AGTACTGGAGTGTTCGAGCATCAAGAGAAACAGTGGTACTGTTTACTGTAACTGATCAAT 541

Qy

488 TTAGAGCGTGGGAAACCTTAGGGATGAATATGGGAAATATGTAAGAGTCCGCGCTTACTG 547

Db

542 TCAAGCATGGCTGCAAAAGGTTTGAACCTGGGTACAATTTGACAGATTACATCTCTG 601

Qy

548 TAGAAGGCTATCAAGTAGCGGAGTGTCTAATGTATATAGCAATACATAGAAATTAACG 607

Db

602 TGGAAAGGTTACCAAGCAGCGGCTCAGCAAAATATAACACAGAAATACATTTACTATTG 661

Qy

608 GT 609

Db

662 GT 663

RESULT 12
AA092876
ID AA092876 standard; DNA; 164 BP.
XX
XX
AC AA092876;
XX
XX
DT 19-APR-1996 (first entry)
XX
XX
DE Thermostable alkaline xylanase gene internal fragment.
XX
XX
KM thermostable alkaline endo-1,4-beta-D-xylanase gene; cloning;
KW polymerase chain reaction; Escherichia coli; EC-3.2.1.8; paper;
KW pulp; bleaching; ds.
XX
XX
OS Bacillus sp. 1-43-3 (CBS672.93).
XX
XX
PN WO9518219-A1.
XX
XX
PD 06-JUL-1995.
XX
XX
PF 23-DEC-1994; 94MO-EP04312.
XX
XX
PR 24-DEC-1993; 93EP-0203694.
XX
XX
PA (KONN) GIST-BROCADES NV.
XX
XX
PI Farrell RL, Goedegebuur F, Herbes WT, Herweijer MA;
PI Iverson S, Jones BE, Quak WJ, Van Beckhoven RFMC;
PI Van der Kleij WA, Van Solingen P, Williams DP;
XX
XX
DR WPI; 1995-246385/32.
XX
XX
PT Novel xylanase enzyme active at high pH - useful in paper and pulp
PT prodn. processes
XX
XX
PS Example 7; Page 40-41; 54pp; English.
XX
XX
CC AA092871-77 are examples of several different internal xylanase gene
CC fragments which were used as specific probes to isolate full length
CC cloned genes. AA092876 is from an G1-type xylanase. The DNA may be
CC cloned in E. coli using a plasmid vector, and e.g. clone KEX106 was
CC isolated, producing 23.7 U/ml recombinant xylanase. The xylanase may be
CC used in the paper and pulp industries, where it produces an increase in
CC ISO brightness of softwood pulp of at least 1.0 over non-enzymatically
CC treated pulp in an ECF pulp bleaching process, at pH 9.0 and 65 deg
CC C. The enzyme may be used in production of paper, board and fluff
CC pulp, and has low cellulase activity. The increased brightness
CC produced using the xylanase allows reduction in the amount of
CC bleaching chemicals used.
XX
XX
SQ Sequence 164 BP; 50 A; 35 C; 39 G; 40 T; 0 other;
XX
XX
Query Match 23.3%; Score 154.4; DB 16; Length 164;
Best Local Similarity 96.3%; Pred. No. 2.7e-36;
Matches 158; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 280 GAAATATTATTTGTGCACAGTTGGGCAACTGGCGTCCACAGAGCAACGCTTAAGGG 339
DB 1 GAATATTATTTGTGCACAGTTGGGCAACTGGCGTCCACAGAGCAACGCTTAAGGG 60
QY 340 ACCATCACTGTTGATGAGAGAACATATGATTTACAGAGCTTTAGATCAATCAACC 399
DB 61 ACCATCACTGTTGATGAGAGAACATATGATTTATGATGAAACTTTAGATCAATCAAGCC 120
QY 400 TCCATTAAAGGGGATTCACATTAAACAATATTGGAGTGTCC 443
DB 121 TCCATTAAAGGGGATTCACATTAAACAATATTGGAGTGTCC 164

RESULT 13
AA092875
ID AA092875 standard; DNA; 164 BP.

XX
XX
AC AA092875;
XX
XX
DT 19-APR-1996 (first entry)
XX
XX
DE Thermostable alkaline xylanase gene internal fragment.
XX
XX
KM thermostable alkaline endo-1,4-beta-D-xylanase gene; cloning;
KW polymerase chain reaction; Escherichia coli; EC-3.2.1.8; paper;
KW pulp; bleaching; ds.
XX
XX
OS Bacillus sp. 1-25-2 (CBS671.93).
XX
XX
PN WO9518219-A1.
XX
XX
PD 06-JUL-1995.
XX
XX
PF 23-DEC-1994; 94MO-EP04312.
XX
XX
PR 24-DEC-1993; 93EP-0203694.
XX
XX
PA (KONN) GIST-BROCADES NV.
XX
XX
PI Farrell RL, Goedegebuur F, Herbes WT, Herweijer MA;
PI Iverson S, Jones BE, Quak WJ, Van Beckhoven RFMC;
PI Van der Kleij WA, Van Solingen P, Williams DP;
XX
XX
DR WPI; 1995-246385/32.
XX
XX
PT Novel xylanase enzyme active at high pH - useful in paper and pulp
PT prodn. processes
XX
XX
PS Example 7; Page 40; 54pp; English.
XX
XX
CC AA092871-77 are examples of several different internal xylanase gene
CC fragments which were used as specific probes to isolate full length
CC cloned genes. AA092875 is from an G-type xylanase. The DNA may be cloned
CC in E. coli using a plasmid vector, and e.g. clone KEX106 was isolated,
CC producing 23.7 U/ml recombinant xylanase. The xylanase may be used in
CC the paper and pulp industries, where it produces an increase in ISO
CC brightness of softwood pulp of at least 1.0 over non-enzymatically
CC treated pulp in an ECF pulp bleaching process, at pH 9.0 and 65 deg
CC C. The enzyme may be used in production of paper, board and fluff
CC pulp, and has low cellulase activity. The increased brightness
CC produced using the xylanase allows reduction in the amount of
CC bleaching chemicals used.
XX
XX
SQ Sequence 164 BP; 50 A; 35 C; 39 G; 40 T; 0 other;
XX
XX
Query Match 22.8%; Score 151.2; DB 16; Length 164;
Best Local Similarity 95.1%; Pred. No. 2.5e-35;
Matches 156; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 280 GAAATATTATTTGTGCACAGTTGGGCAACTGGCGTCCACAGAGCAACGCTTAAGGG 339
DB 1 GAATATTATTTGTGCACAGTTGGGCAACTGGCGTCCACAGAGCAACGCTTAAGGG 60
QY 340 ACCATCACTGTTGATGAGAGAACATATGATTTACAGAGCTTTAGATCAATCAACC 399
DB 61 ACCATCACTGTTGATGAGAGAACATATGATTTATGATGAAACTTTAGATCAATCAAGCC 120
QY 400 TCCATTAAAGGGGATTCACATTAAACAATATTGGAGTGTCC 443
DB 121 TCCATTAAAGGGGATTCACATTAAACAATATTGGAGTGTCC 164

RESULT 14
AA090405
ID AA090405 standard; DNA; 1375 BP.
XX
XX
AC AA090405;
XX
XX
DT 25-MAR-2003 (updated)

DT 28-SEP-1999 (first entry)
 XX Actinomadura sp. DSM43186 35 kDa xylanase encoding DNA.
 DE
 XX
 KW Actinomadura sp. DSM43186; xylanase; Actinomadura flexuosa; lignin;
 KW thermostable; biobleaching; wood pulp; bleaching; hemicellulase;
 KW paper processing; hemicellulose; ss.
 XX
 OS Actinomadura flexuosa.
 XX
 FH Key Location/Qualifiers
 FT CDS 303..1337
 FT /*tag= a
 FT /product= "xylanase"
 XX
 XX US5935836-A.
 XX
 XX 10-AUG-1999.
 XX
 XX 06-JUN-1995; 95US-0468812.
 XX
 XX 06-JUN-1995; 95US-0468812.
 PR 29-JUL-1994; 94US-0282001.
 PR 31-OCT-1994; 94US-0332412.
 PR 31-JUL-1995; 95FI-0003639.
 XX
 PA (ALKO-) ALKO GROUP LTD.
 PA (ALKO-) ALKO-YHTIOET OY.
 PA (ROHM) ROHM ENZYME FINLAND OY.
 XX
 PI Fagerstrom R, Kristo P, Lahtinen T, Lantto R, Maentylae A;
 PI Paloheimo M, Suominen P, Vehmaanperae J;
 XX
 DR WPI; 1996-141347/38.
 DR P-PSDB; AAY24480.
 XX
 XX Actinomadura xylanase sequences and method of use. - No abstract.
 FT
 XX
 PS Disclosure; Fig 13; 54pp; English.
 CC The present invention describes a culture medium obtained from the
 CC culture of a recombinant host cell that is not Actinomadura flexuosa and
 CC has been transformed with a vector encoding a protein having xylanase
 CC activity, where the protein comprises an amino acid sequence from a
 CC xylanolytic fragment of the amino acid sequence in AAY24480 or AAY24481.
 CC Also described is an enzyme preparation derived from the culture medium.
 CC The enzyme composition can be used in a method for biobleaching.
 CC modifying plant biomass properties, especially the reduction of lignin
 CC content in pulp and paper processing. The xylanases are hemicellulases
 CC which partially degrade the hemicellulose and enhance the extractability
 CC of lignins by conventional chemical bleaching of wood pulp. It can be
 CC used alone or as a supplement to other treatments that reduce lignin
 CC content of wood pulp, increase its drainability or decrease its water
 CC retention. The culture medium can be used directly without the need to
 CC purify the enzymes. Actinomadura flexuosa xylanases have a pH optimum
 CC and thermostability desirable for the biobleaching of wood pulp reducing
 CC the need to acidify the pulp prior to xylanase treatment. The xylanases
 CC partially degrade the hemicellulose in wood pulp which enhances the
 CC extractability of lignins by conventional bleaching chemicals and
 CC results in a lower consumption of bleaching chemicals reducing the
 CC formation of environmentally undesired organic compounds. The present
 CC sequence encodes Actinomadura sp. DSM43186 35 kDa xylanase.
 CC N.B. This sequence is indexed from US5935836 which is a treat as
 CC basic specification for F19503639.
 CC (Updated on 25-MAR-2003 to correct DR field.)
 XX
 XX Sequence 1375 BP; 265 A; 517 C; 400 G; 193 T; 0 other;
 SQ
 Query Match 18.0%; Score 119.4; DB 17; Length 1375;
 Best Local Similarity 57.1%; Pred. No. 2.1e-25;
 Matches 238; Conservative 0; Mismatches 176; Indels 3; Gaps 1;
 198 GTCCATAAACTACGGAGCAACTTCCAAACCAATGGTAATCGTATTATTCGCTATGG 257

608 GACCGTGACCTACAAACGCTCTCTTCAACCCGTCGGGTAAACGCTACCTCACGCTCTACGG 667
 258 TTGCACTGTTGACCTCTTGTGCAATATTATTTGTGACAGTTGGGCAACTGGCGTCC 317
 668 CTGACCCAGGAACCGGCTCGTGTGAGTACTATCGTGTGAGAGCTGGGCACTTACCGGCC 727
 318 ACCAGGAGCAACGCTTAAGGGGACCATCCTGTTGTGAGGAGGAACATATGATATCTACGA 377
 728 CACCGG---CACCTACAGGGCACCGTCAACCGAGCGGGGACGTACGACATCTACGA 784
 378 GACTCTTAGAGTCAATCAACCTCTCATTAAGGGGATGCCACATTTAAACAATATTGGAG 437
 785 GACCTGGCGGTACAAACGCGCGCTCCATCGAGGGGACCCCGGACCTTCCAGCAGTTCTGGAG 844
 438 TGTTCGAAGATCGAAACGACGAGTGGCAGCATTTCTGTGAGCAACCACTTTTAGAGCGTG 497
 845 CGTCGGGCGAGAGGCGGACCGGCGACCATTCACCATCGGCAACCACTTCGACGCGCTG 904
 498 GGAATACTTAGGGATGAATATGGGAAATATGAAAGTCCGCTTACTGTAGAGGCTA 557
 905 GGCCGCGCGCATGAACCTGGGCGACGCACTACGAGATCATGGGCGACCGAGGGCTA 964
 558 TCRAAGTAGCGGAAGTCTAATGTATATAGCAATACACTAAGAATTAAACGCTAACCC 614
 965 CCAGAGCAGCGGTAGTCCACCGTCTCCATCAGCGGAGGTGGCAACCCCGCGCAACC 1021

RESULT 15
 AAT64930
 ID AAT64930 standard; DNA; 1375 BP.
 XX
 AC AAT64930;
 XX
 DT 25-MAR-2003 (updated)
 DT 02-APR-1998 (first entry)
 XX
 DE Actinomadura flexuosa 35 kDa (AM35) xylanase encoding DNA.
 XX
 KW Actinomadura flexuosa; xylanase; cellulase; recombinant; fungal host;
 KW pulp; paper industry; enzyme; bleaching; ss.
 XX
 OS Actinomadura flexuosa.
 FH Key Location/Qualifiers
 FT CDS 303..1337
 FT /*tag= a
 FT /product= "AM35 xylanase"
 FT mat_peptide 432..1334
 FT /*tag= b
 XX
 WO9727306-A1.
 XX
 PD 31-JUL-1997.
 XX
 XX 24-JAN-1997; 97WO-FI00037.
 XX
 XX 26-JAN-1996; 96US-0590563.
 XX
 PA (ALKO-) ALKO GROUP LTD.
 XX
 PI Maentylae A, Paloheimo M, Lantto R, Fagerstrom R, Lahtinen T;
 PI Suominen P, Vehmaanperae J;
 XX
 DR WPI; 1997-393693/36;
 DR P-PSDB; AAW23338.
 XX
 PT Production of bacterial proteins, especially xylanase(s) and
 PT cellulase(s) - by recombinant expression in a filamentous fungal
 PT host, useful particularly in the pulp and paper industries.
 XX
 PS Claim 7; Pages 65-67; 127pp; English.
 XX

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OM nucleic - nucleic search, using sw model
Run on: October 20, 2003, 10:40:37 ; Search time 2552 Seconds
(without alignments)
10628.167 Million cell updates/sec

Title: US-09-909-207-1
Perfect score: 663
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	663	100.0	663	6	A48222 Sequence 1
2	663	100.0	663	6	A48223 Sequence 2
3	663	100.0	663	6	AR193049 Sequence
4	663	100.0	663	6	AR193050 Sequence
5	663	100.0	744	6	A48225 Sequence 4
6	663	100.0	744	6	A48226 Sequence 5
7	663	100.0	744	6	AR193051 Sequence
8	663	100.0	744	6	AR193052 Sequence
9	663	100.0	1513	6	A48231 Sequence 10
10	663	100.0	1513	6	A48232 Sequence 11
11	663	100.0	1513	6	AR193055 Sequence
12	663	100.0	1513	6	AR193056 Sequence
13	634.2	95.7	744	6	A68006 Sequence 1
14	634.2	95.7	744	6	AR163110 Sequence
15	624.6	94.2	744	6	A45313 Sequence 18
16	624.6	94.2	744	6	AR117325 Sequence
17	507.8	76.6	744	6	A68016 Sequence 11
18	507.8	76.6	744	6	AR163117 Sequence
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24	274.8	41.4	3493	1	CST508403 Clostridi
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29	255.4	38.5	2364	6	AR203507 Clostridium
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31	255.2	38.5	1022	6	A42285 Sequence 1
32	255.2	38.5	1022	6	AR127019 Sequence
33	255.2	38.5	1022	6	AR127049 Sequence
34	255.2	38.5	1022	6	AR220023 Sequence
35	255.2	38.5	1022	6	AR220053 Sequence
36	255.2	38.5	1022	6	AR221306 Sequence
37	255.2	38.5	1022	6	AR221336 Sequence
38	255	38.5	600	6	A42276 Sequence 26
39	255	38.5	600	6	A42284 Sequence 34
40	255	38.5	600	6	AR127041 Sequence
41	255	38.5	600	6	AR127048 Sequence
42	255	38.5	600	6	AR220045 Sequence
43	255	38.5	600	6	AR220052 Sequence
44	255	38.5	600	6	AR221328 Sequence
45	255	38.5	600	6	AR221335 Sequence

ALIGNMENTS

RESULT 1

A48222
LOCUS A48222
DEFINITION Sequence 1 from Patent (EP0698667).
ACCESSION A48222
VERSION A48222.1
KEYWORDS GI:2302069
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 663)
AUTHORS De, B.E., Lahaye, A., Ledoux, P. and Detroz, R.
TITLE Xylanase, microorganisms for its production, DNA molecules, process of preparation and use thereof
JOURNAL Patent: EP 0698667-A 1 28-FEB-1996;

linear PAT 07-MAR-1997

COMMENT SOLVAY (BE)
Other publication BE 1008751 960702
Other publication BE 1008570 960604
Other publication BR 9503454 960305
Other publication JP 8092284 960409
Other publication FI 953578 960127
Other publication CA 2154628 960127
Other publication AU 2508695 960208.

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BASE COUNT 220 a 131 c 146 g 166 t

ORIGIN

Query Match 100.0%; Score 663; DB 6; Length 663;
Best Local Similarity 100.0%; Pred. No. 1.5e-169; Indels 0; Gaps 0;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 661 AAT 663

RESULT 2 A48223 663 bp DNA linear PART 07-MAR-1997
LOCUS A48223
DEFINITION Sequence 2 from Patent EP0698667.

ACCESSION A48223
VERSION A48223.1 GI:2302070
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
SOLVAY (BE)
Other publication BE 1008751 960702
Other publication BE 1008570 960604
Other publication BR 9503454 960305
Other publication JP 8092284 960409
Other publication FI 953578 960127
Other publication CA 2154628 960127
Other publication AU 2508695 960208.

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BASE COUNT 220 a 131 c 146 g 166 t

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Query Match 100.0%; Score 663; DB 6; Length 663;
Best Local Similarity 100.0%; Pred. No. 1.5e-169; Indels 0; Gaps 0;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CAAATCGTACCGACCAATTCATTTGGCAACACGATGCTATGATTGAAATTTGGAAA 60
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DB 61 GATAGCGGTGCTGGGACCAATGATTCATTCATGCGGCTACCTTCAGTCCCAATGG 120
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 DB 661 AAT 663

RESULT 5

A48225 744 bp DNA linear PAT 07-MAR-1997
 LOCUS Sequence 4 from Patent EP0698667.
 DEFINITION A48225
 ACCESSION A48225
 VERSION A48225.1 GI:2302072
 KEYWORDS
 SOURCE
 ORGANISM

unidentified
 unidentified
 unclassified.

REFERENCE 1 (bases 1 to 744)
 AUTHORS De, B.E., Lahaye, A., Ledoux, P. and Detroz, R.
 TITLE Xylanase, microorganisms for its production, DNA molecules, process
 of preparation and use thereof
 JOURNAL Patent: EP 0698667-A 4 28-FEB-1996;
 SOLVAY (BE)

COMMENT Other publication BE 1008751 960702
 Other publication BE 1008570 960604
 Other publication BR 9503454 960305
 Other publication JP 8092284 960409
 Other publication FI 953578 960127
 Other publication CA 2154628 960127
 Other publication AU 2508695 960208.
 Location/Qualifiers

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BASE COUNT 246 a 144 c 160 g 194 t

Query Match 100.0% Score 663; DB 6; Length 744;
 Beef Local Similarity 100.0%; Pred. No. 1.5e-169;
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 DB 742 AAT 744

RESULT 6

A48226 744 bp DNA linear PAT 07-MAR-1997
 LOCUS Sequence 5 from Patent EP0698667.
 DEFINITION A48226
 ACCESSION A48226
 VERSION A48226.1 GI:2302073
 KEYWORDS
 SOURCE
 ORGANISM

unidentified
 unidentified
 unclassified.

REFERENCE 1 (bases 1 to 744)
 AUTHORS De, B.E., Lahaye, A., Ledoux, P. and Detroz, R.
 TITLE Xylanase, microorganisms for its production, DNA molecules, process
 of preparation and use thereof
 JOURNAL Patent: EP 0698667-A 5 28-FEB-1996;
 SOLVAY (BE)

COMMENT Other publication BE 1008751 960702
 Other publication BE 1008570 960604
 Other publication BR 9503454 960305
 Other publication JP 8092284 960409
 Other publication FI 953578 960127
 Other publication CA 2154628 960127
 Other publication AU 2508695 960208.
 Location/Qualifiers

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Qy	121	AACAATGTTAAACAACATATT	TTCGGTAAGGTAAATAATTC	AAATCAATGAACAACAACACAC	180
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RESULT 7	AR193051	Sequence 4 from patent US 6346407.	744 bp	DNA	linear	PAT 20-APR-2002
LOCUS	AR193051					
DEFINITION	Sequence 4 from patent US 6346407.					
ACCESSION	AR193051					
VERSION	AR193051.1	GI:20239016				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 744)					
AUTHORS	De Buyl, E., Lahaye, A., Ledoux, P. and Detroz, R.					
TITLE	Xylanase, microorganisms producing it, DNA molecules, methods for preparing this xylanase and uses of the latter					
JOURNAL	Patent: US 6346407-A 4 12-FEB-2002;					
FEATURES	Location/Qualifiers					

RESULT 8	AR193052	Sequence 5 from patent US 6346407.	744 bp	DNA	linear	PAT 20-APR-2002
LOCUS	AR193052					
DEFINITION	Sequence 5 from patent US 6346407.					
ACCESSION	AR193052					
VERSION	AR193052.1	GI:20239017				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 744)					
AUTHORS	De Buyl, E., Lahaye, A., Ledoux, P. and Detroz, R.					
TITLE	Xylanase, microorganisms producing it, DNA molecules, methods for preparing this xylanase and uses of the latter					
JOURNAL	Patent: US 6346407-A 5 12-FEB-2002;					
FEATURES	Location/Qualifiers					

RESULT 8	AR193052	Sequence 5 from patent US 6346407.	744 bp	DNA	linear	PAT 20-APR-2002
LOCUS	AR193052					
DEFINITION	Sequence 5 from patent US 6346407.					
ACCESSION	AR193052					
VERSION	AR193052.1	GI:20239017				
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SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 744)					
AUTHORS	De Buyl, E., Lahaye, A., Ledoux, P. and Detroz, R.					
TITLE	xylanase, microorganisms producing it, DNA molecules, methods for preparing this xylanase and uses of the latter					
JOURNAL	Patent: US 6346407-A 5 12-FEB-2002;					

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Location/Qualifiers
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BASE COUNT 246 a 144 c 160 g 194 t
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Query Match 100.0%; Score 663; DB 6; Length 744;
Best Local Similarity 100.0%; Pred. No. 1.5e-169;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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742 AAT 744

RESULT 9

LOCUS A48231 1513 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 10 from Patent EP0698667.
ACCESSION A48231
VERSION A48231.1 GI:2302078
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1513)
AUTHORS De,B.E., Lahaye,A., Ledoux,P. and Detroz,R.
TITLE Xylanase, microorganisms for its production, DNA molecules, process of preparation and use thereof

JOURNAL Patent: EP 0698667-A 10 28-FEB-1996;
SOLVAY (BE)
COMMENT Other publication BE 1008751 960702
Other publication BE 1008570 960604
Other publication BR 9503454 960305
Other publication JP 8092284 960409
Other publication FI 953578 960127
Other publication CA 2154628 960127
Other publication AU 2508695 960208.

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BASE COUNT 500 a 282 c 271 g 460 t
ORIGIN

Query Match 100.0%; Score 663; DB 6; Length 1513;
Best Local Similarity 100.0%; Pred. No. 1.4e-169;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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761 GATACGGTGGCTCTGGGCAATGATTCATTCATTCGCAACCAAGTGGTATGATTAATTTGG 820
121 AACATGTTAAACAATATTTATTCGTTAAAGTAAATTTCAATGAAACAAACACAC 180
821 AACATGTTAAACAATATTTATTCGTTAAAGTAAATTTCAATGAAACAAACACAC 880
181 CAACAAGTTGGTAAATGTCATTAATCTAGAGCACTTCCAAACCAATGTTATGCG 240
881 CAACAAGTTGGTAAATGTCATTAATCTAGAGCACTTCCAAACCAATGTTATGCG 940
241 TATTTATGCGTCTATGTTGATGATCTGTTGACCTCTTTGCAATATTTATTTGCA 300
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421 TTTAAACAATATTTGAGTGTGAAAGTGAAGCAAGCAAGTGGGACGATTTCTGTCA 480
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481 AACCACTTTAGAGCGTGGGAAAATTAGGAGTGAATAGGGGAAAATGTAAGTCGCG 540
1181 AACCACTTTAGAGCGTGGGAAAATTAGGAGTGAATAGGGGAAAATGTAAGTCGCG 1240
541 CTTACTGTAGAGGCTATCAAGTAGCGGAAGTGTATGATATGACAACTACATAAGA 600
1241 CTTACTGTAGAGGCTATCAAGTAGCGGAAGTGTATGATATGACAACTACATAAGA 1300
601 ATTAAAGGTAAACCTCTCTCAACTATTAGTAATGACGAGACGATTAATTGGAATAAA 660
1301 ATTAAAGGTAAACCTCTCTCAACTATTAGTAATGACGAGACGATTAATTGGAATAAA 1360
661 AAT 663
1361 AAT 1363

RESULT 10
LOCUS A48232 1513 bp DNA linear PAT 07-MAR-1997

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DEFINITION Sequence 11 from Patent EP0698667.
ACCESSION A48232
VERSION A48232.1 GI:2302079
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1513)
AUTHORS De,B.E., Lahaye,A., Ledoux,P. and Detroz,R.
TITLE Xylanase, microorganisms for its production, DNA molecules, process
of preparation and use thereof
JOURNAL Patent: EP 0698667-A 11 28-FEB-1996;
SOLVAY (BE)
COMMENT Other publication BE 1008751 960702
Other publication BE 1008570 960604
Other publication BR 9503454 960305
Other publication JP 8092284 960409
Other publication FI 953578 960127
Other publication CA 2154628 960127
Other publication AU 2508695 960208.

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BASE COUNT 500 a 282 c 271 g 460 t
ORIGIN
Query Match 100.0%; Score 663; DB 6; Length 1513;
Best Local Similarity 100.0%; Pred. No. 1.4e-169;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 701 CAAATCGTCACCGACAATTCATTTGGCAACACGATGGCTATGATTATGAATTTTGGAAA 760

Qy 61 GATAGCGGTGGCTCTGGGACAATGATTTCTCAATCATGCGCGGTACGTTTCAGTGCCTCAATGG 120
Db 761 GATAGCGGTGGCTCTGGGACAATGATTTCTCAATCATGCGCGGTACGTTTCAGTGCCTCAATGG 820

Qy 121 AACAAATGTTAACACATATTTATTCCTGTAAGGTAAAAAATTCATATGAACAACAACACAC 180
Db 821 AACAAATGTTAACACATATTTATTCCTGTAAGGTAAAAAATTCATATGAACAACAACACAC 880

Qy 181 CAACAAGTTGGTAACATGTCCTATTAACCTACGAGGACCACTTCCAAACCAATGGTAATGCG 240
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Qy 301 TGGGGCAACTGGCGTCCACAGGAGCAACGCTTAAGGGGACCATCTGTTGATGGAGGA 360
Db 1001 TGGGGCAACTGGCGTCCACAGGAGCAACGCTTAAGGGGACCATCTGTTGATGGAGGA 1060

Qy 361 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCTCCATTAAGGGGATTTGCCACA 420
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Qy 481 AACCACTTTAGAGCGTGGGAAAACCTTAGGGATGAATATGGGAAAATGTATGAAATGCGG 540
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Qy 541 CTTACTGTAGAGGCTATCAAAGTAGCGGAAGTCTTAATGTATATAGCAATACACTAAGA 600
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Qy 661 AAT 663
Db 1361 AAT 1363

RESULT 11
LOCUS AR193055 1513 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 10 from patent US 6346407.
ACCESSION AR193055
VERSION AR193055.1 GI:20239020
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1513)
AUTHORS De Buyl,E., Lahaye,A., Ledoux,P. and Detroz,R.
TITLE Xylanase, microorganisms producing it, DNA molecules, methods for
preparing this xylanase and uses of the latter
JOURNAL Patent: US 6346407-A 10 12-FEB-2002;
FEATURES
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BASE COUNT 500 a 282 c 271 g 460 t
ORIGIN
Query Match 100.0%; Score 663; DB 6; Length 1513;
Best Local Similarity 100.0%; Pred. No. 1.4e-169;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAATCGTCACCGACAATTCATTTGGCAACACGATGGCTATGATTATGAATTTTGGAAA 60
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Qy 61 GATAGCGGTGGCTCTGGGACAATGATTTCTCAATCATGCGCGGTACGTTTCAGTGCCTCAATGG 120
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Qy 121 AACAAATGTTAACACATATTTATTCCTGTAAGGTAAAAAATTCATATGAACAACAACACAC 180
Db 821 AACAAATGTTAACACATATTTATTCCTGTAAGGTAAAAAATTCATATGAACAACAACACAC 880

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Qy 241 TATTTATGCGTCTATGTTGGACTGTTGACCTCTTGTGCGAATATTTATTTGTCGACAGT 300
Db 941 TATTTATGCGTCTATGTTGGACTGTTGACCTCTTGTGCGAATATTTATTTGTCGACAGT 1000

Qy 301 TGGGGCAACTGGCGTCCACAGGAGCAACGCTTAAGGGGACCATCTGTTGATGGAGGA 360
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Qy 361 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCTCCATTAAGGGGATTTGCCACA 420
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DB 1301 ATTAACGGTAACCTCTCTCAACTATTAGTAATAGACGAGACATTAATTGGATAAAAAC 1360
QY 661 AAT 663
DB 1361 AAT 1363

RESULT 12
A6193056 1513 bp DNA linear PAT 20-APR-2002
LOCUS Sequence 11 from patent US 6346407.
DEFINITION A6193056
ACCESSION A6193056
VERSION A6193056.1 GI:20239021
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1513)
AUTHORS De Buy, E., Lahaye, A., Ledoux, P. and Detroz, R.
TITLE Xylanase, microorganisms producing it, DNA molecules, methods for
JOURNAL preparing this xylanase and uses of the latter
FEATURES
source location/Qualifiers
BASE COUNT 500 a 282 c 271 g 460 t
ORIGIN
Query Match 100.0%; Score 663; DB 6; Length 1513;
Best Local Similarity 100.0%; Pred. No. 1.4e-169;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAATCGTACCGCAATTCATTTGGCAACGAGATGGCTATGATGAAATTTGGAAA 60
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QY 61 GATAGCGGTGCTCTGGGCAATGATTTCTCAATCATGAGCGGTACGTTCCAGTCCCAATG 120
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DB 821 AACATGTTAACACATATTTATTCGTAAGGTAAGAAAAATTCATGAAACAAACACAC 880
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DB 1001 TGGGGCAATGCGGTCCACGAGAGCAACGCTTAAGGGGACATCACTGTTGATGAGAGA 1060
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DB 1301 ATTAACGGTAACCTCTCTCAACTATTAGTAATAGACGAGACATTAATTGGATAAAAAC 1360
QY 661 AAT 663
DB 1361 AAT 1363

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RESULT 13
A68006 744 bp DNA linear PAT 05-MAY-1999
LOCUS Sequence 1 from Patent WO9743409.
DEFINITION A68006
ACCESSION A68006
VERSION A68006.1 GI:4756810
KEYWORDS
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 744)
AUTHORS Dalboe, H., Diderichsen, B., Sandal, T. and Kauppinen, S.
TITLE METHOD OF PROVIDING NOVEL DNA SEQUENCES
JOURNAL Patent: WO 9743409-A 1 20-NOV-1997;
NOVONORDISK AS (DK)
FEATURES
source location/Qualifiers
BASE COUNT 249 a 146 c 157 g 192 t
ORIGIN
Query Match 95.7%; Score 634.2; DB 6; Length 744;
Best Local Similarity 97.3%; Pred. No. 1e-161;
Matches 645; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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BASE COUNT 249 a 146 c 157 g 192 t
ORIGIN
Query Match 95.7%; Score 634.2; DB 6; Length 744;
Best Local Similarity 97.3%; Pred. No. 1e-161;
Matches 645; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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DB 202 AACATGTTAACACATATTTATTCGTAAGGTAAGAAAAATTCATGAAACAAACACAC 261

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QY 661 AAT 663
Db 742 AAT 744

RESULT 14
AR163110 LOCUS AR163110 744 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 1 from patent US 6270968.
ACCESSION AR163110
VERSION AR163110.1 GI:16233600
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 744)
AUTHORS Dalb.o slashed.ge,H., Sandal,T., Kauppinen,M.Sakari. and
Diderichsen,Balashedrge.
TITLE Method of providing a hybrid polypeptide exhibiting an activity of
interest
JOURNAL Patent: US 6270968-A 1 07-AUG-2001;
FEATURES Location/Qualifiers
source 1..744
BASE COUNT 249 a 146 c 157 g 192 t
ORIGIN
Query Match 95.7%; Score 634.2; DB 6; Length 744;
Best Local Similarity 97.3%; Pred. No. 1e-161;
Matches 645; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
QY 1 CAATCGTCACCGACAATTCATTCGGCAACCAAGTGGCTATGATTAATGAATTTTGGAAA 60
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Db 622 CTTACTGTAGAGCGTCTCAACTATTAGTATGACGAGAGTAACTTTGATGAAGTAAAC 681
QY 601 ATTAACGGTAAACCCCTCTCAACTATTAGTATGACGAGAGCATAACTTTGATGAAGTAAAC 660
Db 682 ATTAACGGTAAACCCCTCTCAACTATTAGTATGACGAGAGCATAACTTTGATGAAGTAAAC 741
QY 661 AAT 663
Db 742 AAT 744

RESULT 15
AR45313 LOCUS AR45313 744 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 18 from Patent WO9518219.
ACCESSION AR45313
VERSION AR45313.1 GI:2299796
KEYWORDS Unidentified.
SOURCE Unidentified.
ORGANISM Unidentified.
REFERENCE 1 (bases 1 to 744)
AUTHORS Van,S.P., Williams,D.P., Iverson,S., Farrell,R.L., Herbes,W.T.,
Van,D.K., Herweijer,M.A., Van,B.R., Quax,W.J., Goedegebuur,F. and
Jones,B.E.
TITLE ALKALI-TOLERANT XYLANASES
JOURNAL Patent: WO 9518219-A 18 06-JUL-1995;
COMMENT Other publication JP 8507221T 960806
Other publication BR 9405934 951226
Other publication NO 953312 951019
Other publication FI 953920 950821
Other publication AU 1415095 950717.
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BASE COUNT      248 a      145 c      159 g      192 t
ORIGIN

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Query Match      94.2%; Score 624.6; DB 6; Length 744;
Best Local Similarity 96.4%; Pred. No. 4.2e-159;
Matches 639; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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DB      139 GATACGGGTGGCTTGGGACAATGATTCATCATGCGGCTACGTCAGTCCCAATGG 198
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QY      181 CAACAAGTTGTTACATGTCCTAAACTACGAGCCAACTTCCAAACCAATGTTAATGG 240
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QY      361 ACATATGATATTAAGAGCTCTTAGAGTCATCAACCTCCATTAAGGGGATGGCCACA 420
DB      439 ACATATGATATTAAGAGCTCTTAGAGTCATCAACCTCCATTAAGGGGATGGCCACA 498
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QY      481 AACCACTTTAGAGCGTGGGAAAACTTAGGGATGAATATGCGGAAAAATGTATGAAGTCGCG 540
DB      559 AACCACTTTAGAGCGTGGGAAAACTTAGGGATGAATATGCGGAAAAATGTATGAAGTCGCG 618
QY      541 CTTACTGTAGAGCGTATCAAGTAGCGGAAGTGTATATATATGCAATACACTAAGA 600
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QY      601 ATTAACGTTAACCTCTCTCAACTATTAAGTAAGACGAGCATTAATTGGATTAAGAAC 660
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QY      661 AAT 663
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 Job time : 2555 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 20, 2003, 11:28:06 ; Search time 1595 Seconds
(without alignments)
1091.613 Million cell updates/sec

Title: US-09-909-207-1

Perfect score: 663
Sequence: 1 CAATGTCACGCAATTC.....TAATTCGATAAAACAAT 663

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1750203 seqs, 1313063994 residues

Total number of hits satisfying chosen parameters: 3500406

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
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11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
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15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	663	100.0	663	10	US-09-909-207-2
3	663	100.0	744	10	US-09-909-207-4
4	663	100.0	744	10	US-09-909-207-5
5	663	100.0	1513	10	US-09-909-207-10
6	663	100.0	1513	10	US-09-909-207-11
7	119.4	18.0	1375	9	US-09-770-621-1
8	119.4	18.0	1375	12	US-10-286-993-1
9	115.2	17.4	596	12	US-10-307-441-39
10	111.4	16.8	942	14	US-10-213-990-71
11	110	16.6	1002	14	US-10-213-990-70
12	108.8	16.4	705	14	US-10-213-990-68
13	106	16.0	2898	14	US-10-299-393-1
14	104.8	15.8	712	14	US-10-213-990-64
15	103.6	15.6	666	14	US-10-213-990-65
16	96.8	14.6	739	14	US-10-213-990-67

17	86.8	13.1	678	11	US-09-803-454-3	Sequence 3, Appli
18	83.2	12.5	645	12	US-10-237-386-10	Sequence 10, Appl
19	83.2	12.5	657	12	US-10-237-386-11	Sequence 11, Appl
20	79	11.9	2225	11	US-09-790-070A-8	Sequence 8, Appli
21	72.4	10.9	588	12	US-10-237-386-9	Sequence 9, Appli
22	72.4	10.9	983	10	US-09-467-368-1	Sequence 1, Appli
23	54.2	8.2	2054	12	US-10-419-969-5	Sequence 5, Appli
24	50.4	7.6	643	12	US-10-340-860A-39	Sequence 39, Appl
25	41	6.2	74	12	US-10-307-441-24	Sequence 24, Appl
26	40	6.0	557	10	US-09-970-616-1	Sequence 1, Appli
27	38	5.7	6123	12	US-10-311-455-793	Sequence 793, App
28	37.6	5.7	10528	12	US-10-311-455-308	Sequence 308, App
29	36	5.4	787	13	US-10-027-632-13285	Sequence 13285, A
30	36	5.4	8622	12	US-10-311-455-2116	Sequence 2116, Ap
31	35.8	5.4	8880	12	US-09-840-743-10	Sequence 10, Appl
32	35.8	5.4	3673778	12	US-10-312-841-2	Sequence 2, Appli
33	35.6	5.4	478	13	US-10-027-632-63151	Sequence 63151, A
34	35.6	5.4	478	13	US-10-027-632-297516	Sequence 297516,
35	35.6	5.4	5333	8	US-08-781-986A-170	Sequence 170, App
36	35.2	5.3	623	13	US-10-027-632-212128	Sequence 212128,
37	35.2	5.3	980	13	US-10-027-632-9387	Sequence 9387, Ap
38	35.2	5.3	107820	12	US-09-792-616-1	Sequence 1, Appli
39	35	5.3	611	13	US-10-027-632-199892	Sequence 199892,
40	35	5.3	611	13	US-10-027-632-199893	Sequence 199893,
41	35	5.3	10832	12	US-10-311-455-1872	Sequence 1872, Ap
42	34.8	5.2	14307	12	US-10-311-455-701	Sequence 701, App
43	34.8	5.2	17527	12	US-10-311-455-1405	Sequence 1405, Ap
44	34.8	5.2	3673778	12	US-10-312-841-1	Sequence 1, Appli
45	34.6	5.2	5914	12	US-10-311-455-2141	Sequence 2141, Ap

ALIGNMENTS

RESULT 1

US-09-909-207-1
; Sequence 1, Application US/09909207
; Patent No. US20020115181A1
; GENERAL INFORMATION:

APPLICANT: ANDREE LAHAYE
ERIC DE BUYL
PIERRE LEDOUX
RENE DETROZ

TITLE OF INVENTION: Xylanase, microorganisms produced it,
DNA molecule, processes for preparation of this xylanase
and uses thereof

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE

STREET: 2000 K St., N.W., Suite 200

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/909,207

FILING DATE: 19-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/470,953

FILING DATE: 06-JUNE-1995

ATTORNEY/AGENT INFORMATION:

NAME: Wilhem F. Gadiano, Esq.

REGISTRATION NUMBER: 37,136

REFERENCE/DOCKET NUMBER: 4121-40

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-429-0625

TELEFAX: (202) 293-1850

TELEX: 650 383-5605
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 663 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 STRAIN: Bacillus
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-909-207-1

Query Match 100.0%; Score 663; DB 10; Length 663;
 Best Local Similarity 100.0%; Pred. No. 3.1e-186;
 Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAATCGTACCGACAAATTCATTCGACACGACGATGCTATGATTAATTTGGAAA 60
 DB 1 CAAATCGTACCGACAAATTCATTCGACACGACGATGCTATGATTAATTTGGAAA 60
 QY 61 GATACGGTGGCTCTGGGACAAATGATTCATTCATTCGACGATTCAGTCCCAATGG 120
 DB 61 GATACGGTGGCTCTGGGACAAATGATTCATTCATTCGACGATTCAGTCCCAATGG 120
 QY 121 AACAAATGTTAACAAATATTTCCGTAAAGGTAATAAATTCATGAAACAAACACAC 180
 DB 121 AACAAATGTTAACAAATATTTCCGTAAAGGTAATAAATTCATGAAACAAACACAC 180
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 DB 181 CAACAGTTGTTAATGTCATTAATCTGACGACGACGACGACGACGACGACGACGACG 240
 QY 241 TATTTATGCGTCTATGTTGATGATGATGATGATGATGATGATGATGATGATGATG 300
 DB 241 TATTTATGCGTCTATGTTGATGATGATGATGATGATGATGATGATGATGATGATG 300
 QY 301 TGGGGCACTGGCGCTCCACAGAGCAGACGACGACGACGACGACGACGACGACGACG 360
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 QY 361 ACATATGATATCTACGACGACGACGACGACGACGACGACGACGACGACGACGACG 420
 DB 361 ACATATGATATCTACGACGACGACGACGACGACGACGACGACGACGACGACGACG 420
 QY 421 TTTAAACAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
 DB 421 TTTAAACAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
 QY 481 AACCACTTAAAGCGTGGGAAAATTAGGATGATTAATGAGGAAAATGATGATGATG 540
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 DB 601 ATTAAACGTAACCTCTCTCAACTATTAAGTAGAGAGAGATTAATTTGATTAATAAC 660
 QY 661 AAT 663
 DB 661 AAT 663

RESULT 2
 US-09-909-207-2
 Sequence 2, Application US/0909207
 Patent No. US2002015181A1
 GENERAL INFORMATION:
 APPLICANT: ANDREE LAHAYE
 ERIC DE BUYL

PIERRE LEDOUX
 RENE DETROZ
 TITLE OF INVENTION: Xylanase, microorganisms produced it,
 DNA molecule, processes for preparation of this xylanase
 and uses thereof
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: WILHELM BRINKS HOFER GILSON & LIONE
 STREET: 2000 K St., N.W., Suite 200
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20006

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/909,207
 FILING DATE: 19-Jul-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/470,953
 FILING DATE: 06-JUNE-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Wilhem F. Gadiano, Esq.
 REGISTRATION NUMBER: 37,136
 REFERENCE/DOCKET NUMBER: 4121-40
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-428-0625
 TELEFAX: (202) 293-1850
 TELEX: 650 383-5605

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 663 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 STRAIN: Bacillus
 FEATURE:
 NAME/KEY: mat. peptide
 LOCATION: 1..663
 NAME/KEY: CDS
 LOCATION: 1..663
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-909-207-2

Query Match 100.0%; Score 663; DB 10; Length 663;
 Best Local Similarity 100.0%; Pred. No. 3.1e-186;
 Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAATCGTACCGACAAATTCATTCGACACGACGATGCTATGATTAATTTGGAAA 60
 DB 1 CAAATCGTACCGACAAATTCATTCGACACGACGATGCTATGATTAATTTGGAAA 60
 QY 61 GATACGGTGGCTCTGGGACAAATGATTCATTCATTCGACGATTCAGTCCCAATGG 120
 DB 61 GATACGGTGGCTCTGGGACAAATGATTCATTCATTCGACGATTCAGTCCCAATGG 120
 QY 121 AACAAATGTTAACAAATATTTCCGTAAAGGTAATAAATTCATGAAACAAACACAC 180
 DB 121 AACAAATGTTAACAAATATTTCCGTAAAGGTAATAAATTCATGAAACAAACACAC 180
 QY 181 CAACAGTTGTTAATGTCATTAATCTGACGACGACGACGACGACGACGACGACGACG 240
 DB 181 CAACAGTTGTTAATGTCATTAATCTGACGACGACGACGACGACGACGACGACGACG 240
 QY 241 TATTTATGCGTCTATGTTGATGATGATGATGATGATGATGATGATGATGATGATG 300

Db 241 TATTATCGCTCTATGTTGACTGTTGACCCCTCTTGTGCAATATATATATGTCGACAGT 300
Qy 301 TGGGGCAACTCGCGTCCACGAGGACCAACGCTTAAGGGGACCATCACTGTTGTGAGGAGGA 360
Db 301 TGGGGCAACTCGCGTCCACGAGGACCAACGCTTAAGGGGACCATCACTGTTGTGAGGAGGA 360
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Db 361 ACATATGATATCTAGGAGACTCTTAGAGTCAATCAACCCCTCATTAAGGGGATTTGCCACA 420
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Db 421 TTTAAACAATATTTGGAGTGTTCGAAGATCGAAACGACGAGTGGCAGCATTTCTGTGAGC 480
Qy 481 AACCACCTTTAGAGCGTGGGAAAACCTTAGGGATGAATATGCGGAAAATGTATGAAGTCGCG 540
Db 481 AACCACCTTTAGAGCGTGGGAAAACCTTAGGGATGAATATGCGGAAAATGTATGAAGTCGCG 540
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Db 661 AAT 663

RESULT 3

US-09-909-207-4
; Sequence 4, Application US/09909207
; Patent No. US20020115181A1
; GENERAL INFORMATION:
; APPLICANT: ANDREE LAHAYE
; ERIC DE BUYL
; PIERRE LEDOUX
; RENE DETROZ
; TITLE OF INVENTION: Xylanase, microorganisms produced it,
; DNA molecule, processes for preparation of this xylanase
; and uses thereof
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/909,207
; FILING DATE: 19-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/470,953
; FILING DATE: 06-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilhem P. Gadiano, Esq.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-429-0625
; TELEFAX: (202) 293-1850
; TELEX: 650 383-5605
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

LENGTH: 744 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Bacillus
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-909-207-4
Query Match 100.0%; Score 663; DB 10; Length 744;
Best Local Similarity 100.0%; Pred. No. 3.3e-186;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAAATCGTCACCGACAATTCGCAATTCGCAACACGATGGCTATGATTAATTTTGGAAA 60
Db 82 CAAATCGTCACCGACAATTCGCAATTCGCAACACGATGGCTATGATTAATTTTGGAAA 141
Qy 61 GATAGCGGTGGCTCTGGGACAATGATTTCTCAATCATGCGCGTACGTTCAAGTGGCAATGG 120
Db 142 GATAGCGGTGGCTCTGGGACAATGATTTCTCAATCATGCGCGTACGTTCAAGTGGCAATGG 201
Qy 121 AACAAATGTTAAACAATATTTCCGTAAGAGTAAATAATTCATGAAACAACAACACAC 180
Db 202 AACAAATGTTAAACAATATTTCCGTAAGAGTAAATAATTCATGAAACAACAACACAC 261
Qy 181 CAACAAGTTGGTAAACATGTCATAAACTACGGAGCCAACTTCCAACCAAAATGGTAATGCG 240
Db 262 CAACAAGTTGGTAAACATGTCATAAACTACGGAGCCAACTTCCAACCAAAATGGTAATGCG 321
Qy 241 TATTTATGCGTCTATGTTGGACTGTTGACCCCTCTTGTGCAATATTTATTTGTGCAAGT 300
Db 322 TATTTATGCGTCTATGTTGGACTGTTGACCCCTCTTGTGCAATATTTATTTGTGCAAGT 381
Qy 301 TGGGCAACTGGCGTCCACGAGGACCAACGCTTAAGGGGACCATCACTGTTGTGAGGAGA 360
Db 382 TGGGCAACTGGCGTCCACGAGGACCAACGCTTAAGGGGACCATCACTGTTGTGAGGAGA 441
Qy 361 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATTTGCCACA 420
Db 442 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATTTGCCACA 501
Qy 421 TTTAAACAATTTGGAGTGTTCGAAGATCGAAACGACGAGTGGCAGCATTTCTGTGAGC 480
Db 502 TTTAAACAATTTGGAGTGTTCGAAGATCGAAACGACGAGTGGCAGCATTTCTGTGAGC 561
Qy 481 AACCACTTTAGCGCTGGGAAAACCTTAGGATGAATATGGGAAAATGTATGAAGTCGCG 540
Db 562 AACCACTTTAGCGCTGGGAAAACCTTAGGATGAATATGGGAAAATGTATGAAGTCGCG 621
Qy 541 CTTACTGTAGAGGCTATCAAGTAGCGGAAGTCTAATGTATATAGCAATACACTAAGA 600
Db 622 CTTACTGTAGAGGCTATCAAGTAGCGGAAGTCTAATGTATATAGCAATACACTAAGA 681
Qy 601 ATTAACGGTAAACCTCTCTCAACTATTAGTAAATGACGAGACATAAATTTTGGATAAAAAC 660
Db 682 ATTAACGGTAAACCTCTCTCAACTATTAGTAAATGACGAGACATAAATTTTGGATAAAAAC 741
Qy 661 AAT 663
Db 742 AAT 744
RESULT 4
US-09-909-207-5
; Sequence 5, Application US/09909207
; Patent No. US20020115181A1
; GENERAL INFORMATION:
; APPLICANT: ANDREE LAHAYE
; ERIC DE BUYL
; PIERRE LEDOUX
; RENE DETROZ
; TITLE OF INVENTION: Xylanase, microorganisms produced it,

DNA molecule, processes for preparation of this xylanase
and uses thereof

NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSER: WILLIAM BRINKS HOFER GILSON & LIONE
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/909,207
FILING DATE: 19-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/470,953
FILING DATE: 06-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wilhelm F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 744 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Bacillus

FEATURE:
NAME/KEY: CDS
LOCATION: 1..744
NAME/KEY: mat_peptide
LOCATION: 82..744
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1..81
SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-909-207-5

Query Match 100.0%; Score 663; DB 10; Length 744;
Best Local Similarity 100.0%; Pred. No. 3.3e-186;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAATGTCACGCAATTCATTCATGGCAACGAGATGGCTATGATTAATTTGGAAA 60
DB 82 CAAATGTCACGCAATTCATTCATGGCAACGAGATGGCTATGATTAATTTGGAAA 141
QY 61 GATAGGGGTGGCTCTGGGCAATGATTCATTCATGAGGGGTACGTTCAAGTCCCAATGG 120
DB 142 GATAGGGGTGGCTCTGGGCAATGATTCATTCATGAGGGGTACGTTCAAGTCCCAATGG 201
QY 121 AACATGTTAAACAATATATATCCGTAAGAATAAATTCATGAAACACAAACACAC 180
DB 202 AACATGTTAAACAATATATATCCGTAAGAATAAATTCATGAAACACAAACACAC 261
QY 181 CAACAAGTTGTAACATGTCATTAACCTACGAGCCAACTTCCAAACCAATGTTAATGGC 240
DB 262 CAACAAGTTGTAACATGTCATTAACCTACGAGCCAACTTCCAAACCAATGTTAATGGC 321
QY 241 TATTTATGGGTCTAATGTTGAATGTAACCTCTTGTGAATATTAATTTGCGACAGT 300
|||||

DB 322 TATTTATGGGTCTAATGTTGAATGTAACCTCTTGTGAATATTAATTTGCGACAGT 381
QY 301 TGGGGCAACTGGCGCTCCACGAGACCAACGCTTAAGGGAGCACTGTTGATGAGGA 360
DB 382 TGGGGCAACTGGCGCTCCACGAGACCAACGCTTAAGGGAGCACTGTTGATGAGGA 441
QY 361 ACATATGATATTCACGACACTCTTGAAGTCAATCAACCTCCATTAAAGGGATGCCACA 420
DB 442 ACATATGATATTCACGACACTCTTGAAGTCAATCAACCTCCATTAAAGGGATGCCACA 501
QY 421 TTTAAACAATATGAGTGTGGAAGATGGAAGCAGAGGAGGAGCATTTCTGTCAGC 480
DB 502 TTTAAACAATATGAGTGTGGAAGATGGAAGCAGAGGAGGAGCATTTCTGTCAGC 561
QY 481 AACCACTTTAGAGCGCTGGGAAAACTTAGGATGATATGAGGAAAAATGATGAGTCCGC 540
DB 562 AACCACTTTAGAGCGCTGGGAAAACTTAGGATGATATGAGGAAAAATGATGAGTCCGC 621
QY 541 CTACTGTGAAGGCTATCAAAAGTACGGAAGTCTAATGTATATGCAATACCTAAGA 600
DB 622 CTACTGTGAAGGCTATCAAAAGTACGGAAGTCTAATGTATATGCAATACCTAAGA 681
QY 601 ATTAACGGTAACCTCTCTCAACTATTAATGATGACGAGCATPACTTGGATAAAC 660
DB 682 ATTAACGGTAACCTCTCTCAACTATTAATGATGACGAGCATPACTTGGATAAAC 741
QY 661 AAT 663
DB 742 AAT 744

RESULT 5
US-09-909-207-10
Sequence 10, Application US/09909207
Patent No. US20020115181A1
GENERAL INFORMATION:
APPLICANT: ANDRÉE LAHAYE
ERIC DE BUYL
PIERRE LEDOUX
RENE DETROZ
TITLE OF INVENTION: Xylanase, microorganisms produced by it,
DNA molecule, processes for preparation of this xylanase
and uses thereof

NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSER: WILLIAM BRINKS HOFER GILSON & LIONE
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006

COMPUTER READABLE FORM:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/909,207
FILING DATE: 19-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/470,953
FILING DATE: 06-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wilhelm F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:

Db	941	TATTATTCGGCTTATGTTGGACTGTGGACCTCTGTGCAATATTAATTTGTGCACGT	1000
Oy	301	TGGGGCAACTGGCGTCCACAGAGCAACGCTTAAGGGACCATCACTGTTGATGAGGA	360
Db	1001	TGGGGCAACTGGCGTCCACAGAGCAACGCTTAAGGGACCATCACTGTTGATGAGGA	1060
Oy	361	ACATATGATATCTACGAGACTCTTGAAGTCAATCAACCTTCATTAAGGGATTGCCACA	420
Db	1061	ACATATGATATCTACGAGACTCTTGAAGTCAATCAACCTTCATTAAGGGATTGCCACA	1120
Oy	421	TTTAAACAATTTGGAGTGTTCGAAGATCGAAACGCAAGTGGCAGATTTCTGTACGC	480
Db	1121	TTTAAACAATTTGGAGTGTTCGAAGATCGAAACGCAAGTGGCAGATTTCTGTACGC	1180
Oy	481	AACCACTTAAAGCTGGGAAAACCTTAGGATGAATATGGGGAAAATGTATGAAGTCGCG	540
Db	1181	AACCACTTAAAGCTGGGAAAACCTTAGGATGAATATGGGGAAAATGTATGAAGTCGCG	1240
Oy	541	CTTACTGTAGAAGCTATCAAAAGTAGCGGAAGTGTATGTATATAGCAATACACTAGA	600
Db	1241	CTTACTGTAGAAGCTATCAAAAGTAGCGGAAGTGTATGTATATAGCAATACACTAGA	1300
Oy	601	ATTAAAGGTAAACCCCTCTCAACTTATGTATAGCGAGCATTAACCTTGGATTAANAAC	660
Db	1301	ATTAAAGGTAAACCCCTCTCAACTTATGTATAGCGAGCATTAACCTTGGATTAANAAC	1360
Oy	661	AAT 663	
Db	1361	AAT 1363	

RESULT 7
 US-09-770-621-1
 : Sequence 1, Application US/09770621
 : Patent No. US20010024815A1
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: M nlyi, Arja
 : APPLICANT: Venhaaper, Jari
 : APPLICANT: Fagerstr m, Richard
 : APPLICANT: Lantto, Raija
 : APPLICANT: Paloheimo, Marja
 : APPLICANT: Suominen, Pirkko
 : APPLICANT: Lehtinen, Tarja
 :
 : TITLE OF INVENTION: Production and Secretion of Proteins of
 :
 : NUMBER OF SEQUENCES: 39
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
 : STREET: 1100 New York Ave., N.W. Suite 600
 : CITY: Washington
 : STATE: D.C.
 : COUNTRY: U.S.A.
 : ZIP: 20005
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent in Release #1.0, Version #1.30
 :
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/770,621
 : FILING DATE:
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/590,563
 : FILING DATE:
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/332,412
 : FILING DATE: 31-OCT-1994
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/282,001
 : FILING DATE: 29-JUL-1994
 : CLASSIFICATION:

```

1  ATTORNEY/AGENT INFORMATION:
2  NAME: Bugalsky, Lawrence B.
3  REGISTRATION NUMBER: 35, 086
4  REFERENCE/DOCKET NUMBER: 1050.0340003
5  TELECOMMUNICATION INFORMATION:
6  TELEPHONE: 202-371-2600
7  TELEFAX: 202-371-2540
8  INFORMATION FOR SEQ ID NO: 1:
9  SEQUENCE CHARACTERISTICS:
10 LENGTH: 1375 base pairs
11 TYPE: nucleic acid
12 STRADENESS: No. US20010024815A1 Relevant
13 TOPOLOGY: linear
14 MOLECULE TYPE: DNA (genomic)
15 FEATURE:
16 NAME/KEY: CDS
17 LOCATION: 303..1334
18
19 US-09-770-621-1

```

Query Match	18.0%;	Score 119.4;	DB 9;	Length 1375;
Best Local Similarity	57.1%;	Pred. No. 8.2e-25;		
Matches 238;	Conservative 0;	Mismatches 176;	Indels 3;	Gaps 1

Oy	198	GTCCATAAATCTAGAGGCCAATTCACCAACAAATGGTAATCGAATTATTAAGCGTAAATGG	257
Db	608	GACCTGACCTACAAAGCCTCTTTAAACCCGTGGGTACGGGTCACTCAACGCTTACGG	667
Oy	258	TTGAGATGTTGACCCCTTTTGCAATATTATATTTGTCAGAGTTGGGGCAACTGGCGTCC	317
Db	668	CTGGACCAAGGAACCGCTGTGTGAGTACTACGTGTGAGAGTGTGGGGCACTTACCGGCC	727
Oy	318	ACCAGAGCAACGCCCTTAAGGGGACCATCATCTGTTGATGAGAGGAACATTTGATTTACGA	377
Db	728	CACCGG---CACCTACAGGGGACCGGTACACCGACGGGGGAAGTACGACATCTACGA	784
Oy	378	GACCTTAAGTCAATCAACCCCTCATTTAAAGGGGATTTCCACATTTTAAACAATTTGGAG	437
Db	785	GACCTGGCGGTACAAAGCGCGCTCCATGAGGGGACCCGGACCTTCCAGAGTTCTGGAG	844
Oy	438	TGTTGAAAGATCGAACAACGACAGATGGGACGATTTCTGTGACAGCAACTTTAGAGCGTG	497
Db	845	CGTCCGGCAGAGAAACGGACAGGGGACCATCATCTCGGCAACCACTTCGACGCGCTG	904
Oy	498	GGAAAACTTAGGGATGATATATGGGGAAAAATGATATGAACTCGCGCTTACTGTGAAGGCTA	557
Db	905	GGCGCCGCGCGGATATMACCTTGGGACGCCACGACTTACAGATTCATGGCGAACCGGAGGCTA	964
Oy	558	TCAAAGTAGGGAAGGCTAATGTATATTAAGCAATCACTAAGAAATTAAAGGTAAAGCC	614
Db	965	CGAAGAGAGGGATGCTTCCACCGCTTCCATATCAGCGAGGGTGGCAACCCCGGCAACCC	1021

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RESULT 8
US-10-286-993-1
; Sequence 1, Application US/10286993
; Publication No. US2003014845A1
; GENERAL INFORMATION:
; APPLICANT: Mantyla, Arja
; APPLICANT: Paloheimo, Maria
; APPLICANT: Lantto, Raija
; APPLICANT: Fagerstrom, Richard
; APPLICANT: Lahtinen, Tarja
; APPLICANT: Suominen, Pirkko
; APPLICANT: Vehmaanpera, Jari
; TITLE OF INVENTION: Production and Secretion of Proteins in Filamentous
; TITLE OF INVENTION: Fungi
; FILE REFERENCE: 1716.0340004
; CURRENT APPLICATION NUMBER: US/10/286,993
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/120,804
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: FCT/ET97/00037
; PRIOR FILING DATE: 1997-01-24

```

; PRIOR APPLICATION NUMBER: US 08/590,563
; PRIOR FILING DATE: 1996-01-26
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1375
; TYPE: DNA
; ORGANISM: Actinomyces flexuosus (Strain: DSM43186)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (303)..(1337)
; OTHER INFORMATION: Product= AM35 xylanase
US-10-286-993-1

Query Match 18.0%; Score 119.4; DB 12; Length 1375;
Best Local Similarity 57.1%; Pred. No. 8.2e-25;
Matches 238; Conservative 0; Mismatches 176; Indels 3; Gaps 1;

Oy 198 GTCCATAAATACGAGCAACTTCCAAACCAATGGTAATGGTATTTATGGCTATGG 257
Db GACCGTGACCTACAAACGCTCTCTCAACCCGTCGGGTAAACGGCTACCTCACGCTCTACGG 667
Oy 258 TTGACTGTGACCTCTTGTGGAATATTATATTGTCGACAGTTGGGCAACTGGCGTCC 317
Db CTGGACCAAGAACCGCTCGTGTGAGTACTATCTGTCGAGCTGGGGCACTTACCGGCC 727
Oy 318 ACCAGGACCAACGCTTAAGGGGACCACTCACTGTTGATGGAGGAACATATGATCTACGA 377
Db CACCGG---CACCTAAGAGGCAACCGTCAACACGAGCGGGGACGTAACGATCTACGA 784
Oy 378 GACTCTTAGAGTCAATCAACCTCTCAATTAAGGGGATTCGCACATTAACCAATATTGGAG 437
Db GACTTGGCGGTACAAACGCGCGCTCCATCGAGGGGCAACCGGACCTTCCAGCAGTTCTGGAG 844
Oy 438 TGTTCGAAGATCGAAACGACGAGTGGCAGCATTTCTGTGACCAACCACTTTAGAGCGTG 497
Db CGTGGGAGAGAGCGGACGAGCGGACCATACCATCGGCAACCACTTCGAGCGCTG 904
Oy 498 GAAACATTTAGGATGAATATGGGAAATGTATGAAGTCGCGCTTACTGTAGAGGCTA 557
Db GCGCGCGCGCATGAACCTGGGAGCAGCAGCTACCATGATGAGCGGAGGCTA 964
Oy 558 TCAAGTACGGAAGTGTATGTATATAGCAATACATAGATTAACGGAACCC 614
Db CCAGAGCAGCGTAGCTCCACCGTCTCCATCATGAGGAGGTGGCAACCCCGGCAACCC 1021

RESULT 9

US-10-307-441-39
; Sequence 39, Application US/10307441
; Publication No. US20030166236A1
; GENERAL INFORMATION:
; APPLICANT: SUNG, Wing L.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity
; TITLE OF INVENTION: and Alkalophilicity
; FILE REFERENCE: 027367-5006US
; CURRENT APPLICATION NUMBER: US/10/307,441
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: PCT/CA01/00769
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/213,803
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Trx
US-10-307-441-39

Query Match 17.4%; Score 115.2; DB 12; Length 596;
Best Local Similarity 57.7%; Pred. No. 9.3e-24;
Matches 226; Conservative 0; Mismatches 163; Indels 3; Gaps 1;
Oy 193 AACATGTCCATAAATACGAGCAACTTCCAAACCAATGGTAATGGTATTTATGGCTC 252
Db AATAAGTGTATCAACTCTCTGTGATCTTATAATCCGAATGGGAATTCATCTTAAGCGTC 250
Oy 253 TATGTTGGACTGTTGACCTCTTGTGGAATATTATATTGTGACAGTTGGGGCAACTGG 312
Db TATGCTGTTCTAGAAACCCACTGATTGAATATTACATTGTGGAATTTTCGGTACCTAC 310
Oy 313 CGTCC---ACCAGAGCAACGCTTAAGGGGACCATCACTGTTGATGGAGGAACATATGAT 369
Db AATCCGAGTAGTCGGCGGCCACAAATATTAGGGGAAGTCACTAGTGTGATCCGTATATGAT 370
Oy 370 ATCTACGAGACTCTTAGAGTCAATCAACCTTCAATTAAGGGGATTCACACATTTAAACAA 429
Db ATCTACGATCCCAACCGGTTAATCAGCATCGATCATTTGGAACCGCACCTTTTATCAG 430
Oy 430 TATTGGAGTGTTCGAAGATCGAAACGACGAGTGGCAGATTTCTGTGACCAACCACTTT 489
Db TACTGGAGTGTAGACGTAATCATCGGAGCTCCGGTTCGGTTAATCTGCGAATCACTTT 490
Oy 490 AGAGCGTGGGAAACTTAGGGATGAATATGGGGAATATGATGAAGTCGCGCTTACTGTA 549
Db AATGCATGGGCACAGCAAGGGTTAAACCTAGGTACAAATGGAATATCAAAATCGTAGCGGTG 550
Oy 550 GAAGCGTATCAAGTAGCGGAAGTGCTAATGT 581
Db GAAGCGTACTTCTCGAGTGGTTCGCTAGTAT 582

RESULT 10

US-10-213-990-71
; Sequence 71, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Bussey, Howard
; APPLICANT: Jiang, Bo
; APPLICANT: Storms, Reg
; APPLICANT: Rosner, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; TITLE OF INVENTION: ENZYMES AND METHODS OF USE
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 942
; TYPE: DNA
; ORGANISM: Aspergillus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(942)
US-10-213-990-71

Query Match 16.8%; Score 111.4; DB 14; Length 942;
Best Local Similarity 57.0%; Pred. No. 1.6e-22;
Matches 224; Conservative 0; Mismatches 166; Indels 3; Gaps 1;
Oy 182 AACAAAGTTGGTAACATGTCCATAAATACGAGGCAACTTCCAAACCAATGGTAATGGT 241
Db ATCCAGGAGTGACCATGACATTTACCTTCTTGGCAGCTTCATCTTCCGGAATGCTT 316
Oy 242 ATTTATCGCTATGTTGAGCTGTTGACCTCTTGTGGAATATTATATTGTCGACAGTT 301
Db ACCTGTCGCTATGATGATGGAGTACCAACCCCTTAGTTCGAATACTACATCTCCGGAAC 376
Oy 302 GGGGCA---ACTGGCGTCCACGAGCAACGCTTAAGGGGACCATCACTGTTGATGAG 358
Db ATGGCAGTTAAATCTTGGCTCGGCGCATGACGCAAGGGGACCGTCACCAGCGATGAT 436

Query 11
US-10-213-990-70
Sequence 70, Application US/10213990
Publication No. US20030082595A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
FILE REFERENCE: 10182-019-999
CURRENT APPLICATION NUMBER: US/10/213,990
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 70
LENGTH: 1002
TYPE: DNA
ORGANISM: Aspergillus
US-10-213-990-70

Query Match
Best Local Similarity 57.8%; Score 110; DB 14; Length 1002;
Matches 216; Conservative 0; Mismatches 155; Indels 3; Gaps 1;

359 GAACATGATATCTAGAGACTCTTGAATCAACCTTCATTAAAGGGGATTGCCA 418
437 CCACCTAGACATCTATGAGCAACCAAGAGCTTCATCGTCGACAGGCCA 496
419 CATTAAACAAATTTGAGTGTTCGAAGATCGAAACGACAGTGGCAGATTTCTGCA 478
497 CCTTCAACCAATATCTGTCATCCGCAAAACAGGATCCAGCGGACAGTCAACCG 556
479 GCAACCACTTTAGAGCGTGGGAAAATTAGGATGATATGAGGAAATGATGAAGTCG 538
557 CGAATCACTTCAAGGCTGGGCTAGTCTGGGATGAACTGGGTACCAATCACTATCACA 616
539 CGCTTACTGTAGAGGCTATCAAAGTAGCGGAA 571
617 TTGTTCCACTAGAGGATATGAGACGCGGTA 649

RESULT 12
US-10-213-990-68
Sequence 68, Application US/10213990
Publication No. US20030082595A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
FILE REFERENCE: 10182-019-999
CURRENT APPLICATION NUMBER: US/10/213,990
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 68
LENGTH: 705
TYPE: DNA
ORGANISM: Aspergillus
FEATURE:
NAME/KEY: CDS
LOCATION: (1) ... (705)
US-10-213-990-68

Query Match
Best Local Similarity 51.9%; Score 108.8; DB 14; Length 705;
Matches 298; Conservative 0; Mismatches 267; Indels 9; Gaps 2;

6 GSTACCGCAATTCATTTGGCAACACAGATGGGTATATGATTTGGAAAGATAG 65
120 CGGACCCCAAGCTTCCAGCGGTGGACACAGGCTACTACTCTTCTGAGCTGATGG 179
66 CGGTGCTCTGAGCAATGATTTCTCAATCATGCGGCTAGCTTCACTGATGCCAATGACAA 125
180 CGGCGGCAAGTGAATCTACACCAATGCGCGGTGCTGATCTCCGTCACTGAGGAA 239
126 TGTAAACAATATTATTCCTTAAGGTAATAAATTCATGAACAAACACACCAACA 185
240 CGTGGCAACTTTTGTGCGTGAAGAGGC-----TGAAACCTGGAGCGCTAGGTACCG 293
186 AGTTGTAACATGTCATTAACCTACGAGCAACTTCACCAATGTAATGCGTATTT 245
294 AGCTTAACTGAACATCACTACGAGGAGCTTCAACCCACGCGCAATGGCTACT 353
246 ATGCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 305
354 GGTGTCTACGCTGAGACCAACACCCCTTATGATGATGATGATGATGATGATGATG 413
306 CA---ACTGGGCTCCACAGAGCAAGCCCTAAGGGGACATCACTGTTGATGAGGAAC 362
414 TACATTAACACCCCGGACAGCGGCTTCACTTCAAGGGGACATCAACCGAGCGTGGAC 473
363 ATATGATATCTACAGAGCTCTTAAAGTCAATCAACCTTCATTAAAGGGGATTCACATT 422
474 TTCAACATCTACAGCGCGCTTCTTCAATGCTTCTTCAATGAGGACCAAGACCTT 533
423 TAAACATATGAGTGTGTCGAAGATCGAAACGACAGAGTGGCAAGATTTCTGACGAA 482
534 CACCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 593
483 CCACTTTAGAGCGTGGGAAAATTAGGATGATATGAGGAAATGATGATGATGATGATG 542
594 CCACTTTCAAGCTGGGACAGATGAGGATGATGATGATGATGATGATGATGATGATG 653
543 TACTGTAGAGGCTATCAAGTAGGGAAGTCT 576
654 CGCACTAGAGGATTAACAGAGAGGATCTGCT 687

RESULT 13
US-10-299-393-1
Sequence 1, Application US/10299393

RESULT 14
US-10-213-990-64
; Sequence 64, Application US/10213990

/ NAME/KEY: CDS
/ LOCATION: (1)...(666)
US-10-213-990-65

Query Match 15 6%; Score 103.6; DB 14; Length 666;
Best Local Similarity 56.3%; Pred. No. 2.7e-20;
Matches 215; Conservative 0; Mismatches 164; Indels 3; Gaps 1;

Qy	203 TAACTACGAGCCCACTTCAACCAATGTATGCGTATTATGCGTCTATGTTGA	262
Db	272 TCACCTACGAGCGGCTCTCGGACAGGGAAGGCTACCTCTCGTACGGCTGA	331
Qy	263 CTGTTGACCTCTTGTGAAATTTATATTGTGACAGTTGGGCAACTGGCTCCACA	321
Db	332 CGACCAATCGCTGTGGAATTTACATGCTGAGAGTTACGGCTCTTATGACCCCTCCA	391
Qy	322 --GGAGCAACGGCTAAGGGGACCATGCTTTGATGAGGAAATATGATATCTACGAGA	379
Db	392 CGGAGCCACCACTCTGGCACCGTCGAGAGCGACGGGCGACGTACAACTCTACAGAA	451
Qy	380 CTCTTAGAGTCAATCAACCTCCATTAGGGGATTCACATTTAAACAATATTGGAGTG	439
Db	452 CGACCGGACGAATGGCGGCTCATCCAGGGCACGGCTACTTTGACAGTACTGGTCGG	511
Qy	440 TTGGAAGATCGAAGCGCAGAGTGGCAGATTTCTGTACCAACCACTTTAGAGCTGGG	499
Db	512 TTCGGACTTCGCAACCGGACAGTGGAACTGTGACGAGAAACCACTTTGATGCGTGA	571
Qy	500 AAACTTAGGATGAAATATGGGAAATATGATGAAGTCGCGCTTACTGTAGAAGCTATC	559
Db	572 GAAATCGGGTCTGCAATTGGGAACTTGACTATATGATTTGTTGACGAGGGGTACC	631
Qy	560 AAAGTAGCGGAAGTCTAATGT	581
Db	632 AGAGCAGCGGCTCTGCTACTAT	653

Search completed: October 20, 2003, 13:35:44
Job time : 1600 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 20, 2003, 10:40:41 ; Search time 2045 Seconds
(without alignments)
7879.642 Million cell updates/sec

Title: US-09-909-207-1
Perfect score: 663
Sequence: 1 CAATGTCACCGAATTC.....TAATTTGGATAAAAACAAT 663

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
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5: em_estov:*
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8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hrc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
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25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86.6	13.1	738	14	CD464145
2	83.4	12.6	921	14	CD458837
C 3	82.8	12.5	603	28	AQ160513
C 4	82.2	12.4	670	28	AQ447125

C 5	82.2	12.4	720	28	AQ361561
C 6	82.2	12.4	750	28	AQ160254
C 7	81.6	12.3	786	28	AQ325248
C 8	81.4	12.3	583	28	AQ399120
C 9	76.6	11.6	561	28	AQ396475
C 10	74.6	11.3	753	28	AQ448084
C 11	74.4	11.2	418	28	AQ398756
C 12	69.8	10.5	520	13	BQ165950
C 13	66.2	10.0	561	13	BQ471960
C 14	63.2	9.5	473	14	CD464005
C 15	60.4	9.1	483	13	BQ664593
C 16	53.6	8.1	646	28	AQ449078
C 17	49.4	7.5	490	10	BF200865
C 18	46.4	7.0	532	12	BM134812
C 19	46.6	7.0	503	13	BQ166480
C 20	45.2	6.8	587	14	CD033274
C 21	41.6	6.3	488	12	BM135798
C 22	40.2	6.1	665	10	BB664921
C 23	40.2	6.1	1319	11	AK053390
C 24	39.6	6.0	704	13	BQ110128
C 25	39	5.9	1146	13	BX446722
C 26	38.8	5.9	588	28	AQ630020
C 27	38.8	5.9	750	14	CA447770
C 28	38.8	5.9	1809	11	BC022353
C 29	38.2	5.8	615	28	AZ059161
C 30	38	5.7	540	12	BM897662
C 31	38	5.7	933	29	CNS01TBY
C 32	37.6	5.7	279	10	BB430376
C 33	37.2	5.6	403	28	AQ461126
C 34	37.2	5.6	861	29	CNS0117J
C 35	37	5.6	690	28	BZ023864
C 36	37	5.6	702	28	BH938430
C 37	36.8	5.6	646	14	CB160626
C 38	36.8	5.6	1101	29	CNS01616
C 39	36.6	5.5	232	9	AV315991
C 40	36.6	5.5	437	12	BM107570
C 41	36.6	5.5	549	14	N20977
C 42	36.6	5.5	685	28	BH989520
C 43	36.6	5.5	698	29	AG007299
C 44	36.6	5.5	705	29	AG007300
C 45	36.6	5.5	714	28	BZ045202

ALIGNMENTS

RESULT 1
CD464145
LOCUS
DEFINITION
ETH1_48_B06.g1_A002 Ethylene-treated seedlings Sorghum bicolor CDNA
clone ETH1_48_B06_A002 5', mRNA sequence.
CD464145
VERSION
CD464145.1 GI:31385413
KEYWORDS
EST.
SOURCE
Sorghum bicolor (sorghum)
ORGANISM
Sorghum bicolor
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE
AUTHORS
Cordonnier-Pratt,M.-M., Wentzel,V., Suzuki,Y., Sugano,S., Klein
N., Liang,C., Sun,F., Sullivan,R., Shah,M., Salzman,R., Chua Tan
N., Gonzalez,M., Lane,S., Miller,V., Nanda,P., Olaseinde,O.,
Eastman,A. and Pratt,L.H.
TITLE
An EST database from Sorghum: 1-aminocyclopropane-1-carboxylic acid
(ACC)-treated seedlings
JOURNAL
Unpublished
COMMENT
Other ESTs: ETH1_48_B06.bi_A002
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860

Fax: 706 583 0210
Email: mmpirat@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; plant material and RNA prepared at Texas A & M University; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.

Seq primer: Sug5 (CTCTGCTCAAAAGTCGC).

FEATURES

source

Location/Qualifiers

1..738
/organism="Sorghum bicolor"
/mol_type="mRNA"
/cultivar="BTx623"
/db_xref="taxon:4558"
/clone="ETH1.48.B06.A002"
/lab_host="DH10B-T1 phage-resistant E. coli"
/note="Ethylene-treated seedlings"
/note="Vector: pMB18-F13; Site 1: XhoI; Site 2: XhoI; The library was prepared from polyA+ RNA from seedlings grown in hydroponic culture. At 8 days of age, medium was supplemented with 0.5 mM 1-aminocyclopropane-1-carboxylic acid (ACC) to induce endogenous ethylene (ETH) production. Roots and shoots were harvested after 27 and 72 hr and material from both time points was combined prior to RNA isolation. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pMB18-F13 vector (5'-prime DraIII site is CACGCGG, 3'-prime DraIII site is CACCATGTC). XhoI excises the cDNA insert."

BASE COUNT

168 a 242 c 164 g 164 t

ORIGIN

Query Match 13.1%; Score 86.6; DB 14; Length 738;

Best Local Similarity 53.5%; Pred. No. 2.7e-09; Mismatches 174; Indels 3; Gaps 1;

Matches 204; Conservative 0; Mismatches 174; Indels 3; Gaps 1;

200 CCATAAATACGAGCACTTCCAAACCAATGTAATCGATTATTCGCTATGTT 259
345 CCATCAAGTACTCTGTACTTCAACATCAAGCAAGCTACCTCGCTTTAGGAT 404
260 GGAAGTGTGACCTCTTGTGAAATTTATTTGTGACAGTTGGGCAACTGGCTCCAC 319
405 GGACTCAGAACCTCTCATCGAGTACTACATCGTTGAGAACTTCGACCTCAACCCCT 464
320 CA---GAGCAAGCGCTAAGGGGACCATGCTGTGATGAGGAAATATGATATACG 376
465 CTTCCGGCCGCGAAGAAAGGGAGGAGTCACTGTGACGATCTGTTCAGACATCTACG 524
377 AGACTTTAGTCAATCAACCTCCATTAAAGGGGATTCACATTTAAACAATTTGA 436
525 TCAGACACCGGTGTCAACGCCCTTCATTGAGGGTAAACAAGCCTTTCAGAGTTGGT 584
437 GTGTTGAAGATCGAAAGCAGAGTGCACGATTTCTGTCAAGCAACCTTTAGAGCT 496
585 CTGTTGAGCGCAACAGCGATCCAGCGATCCGTCACACCGGTGCTCAAGGCT 644
497 GGGAAACTTAGGATGATGAGGAAATGTATGATGATGATGATGATGATGATGATGAT 556
645 GGAAGAAATGTGCGCTCAACCTTGTGACCAACATGATGATGATGATGATGATGATGAT 704
557 ATCAAGTAGCGAAGTGTCTA 577
705 ACTACAGCTCTGCTCTGCA 725

RESULT 2
CD458837 921 bp mRNA linear EST 03-JUN-2003
LOCUS Fg08_04b10_A Fg08 AFRC ECORC Fusarium graminearum complex_substrate
DEFINITION Gibberella zeae cDNA clone Fg08_04b10, mRNA sequence.

ACCESSION CD458837
VERSION CD458837.1 GI:31373577
KEYWORDS EST.
SOURCE Gibberella zeae
ORGANISM Gibberella zeae
REFERENCE Hypocymycetidae; Hypocreales; Nectriaceae; Gibberella.
AUTHORS Watson,R.J., Heyes,R., Chapados,J., Couroux,P., Harris,L.J., Hartori
1 (bases 1 to 921)
J., Lacroix,C., Ouellet,T., Robert,L.S., Singh,J.A., Sprott,D. and
Tinker,N.A.

TITLE

A cDNA library prepared from Fusarium graminearum grown on a

complex plant substrate

JOURNAL

Unpublished
Contact: Watson, Robert.J.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 20, Central Experimental Farm, Ottawa, Ontario, K1A 0C6,
CANADA
Tel: (613) 759-1655
Fax: (613) 759-1701
Email: watsonrj@agr.gc.ca.

FEATURES

source

Location/Qualifiers

1..921
/organism="Gibberella zeae"
/mol_type="mRNA"
/strain="DAOM 180378"
/db_xref="taxon:5518"
/clone="Fg08_04b10"
/tissue="Fusarium"
/dev_stage="Asexual"
/lab_host="E. coli DH10B"
/clone_11b="Fg08 AFRC ECORC Fusarium graminearum complex_s
ubstrate"
/note="Vector: pBluescript II+; Site 1: EcoRI; Site 2:
XhoI; Fusarium graminearum grown on a complex plant
substrate-- wheat leaves treated to remove most of the low
molecular weight, water-soluble components."

BASE COUNT

203 a 254 c 232 g

ORIGIN

Query Match 12.6%; Score 83.4; DB 14; Length 921;

Best Local Similarity 52.4%; Pred. No. 1.4e-08; Mismatches 186; Indels 3; Gaps 1;

Matches 208; Conservative 0; Mismatches 186; Indels 3; Gaps 1;

200 CCATAAATACGAGCACTTCCAAACCAATGTAATCGATTATTCGCTATGTT 259
363 CCATCAAGTACTCTGTACTTCAACATCAAGCAAGCTACCTCGCTTTAGGAT 422
260 GGAAGTGTGACCTCTTGTGAAATTTATTTGTGACAGTTGGGCAACTGGCTCCAC 319
423 GGACCCGGGCTCCCTGTGAGTACTACGATGAGATTAACGTTCTTCAACACCCG 482
320 CAGGA---GCAAGCGCTAAGGGGACCATCACTGTTGATGAGGAAATATGATATCTACG 376
483 GGACGAGGCTTAGACCGAGGTACCTGTACACCGAGGTACCTTAGATCTCTATA 542
377 AGACTTTAGTCAATCAACCTCCATTAAAGGGGATTCACATTTAAACAATTTGA 436
543 TGTCAACCGGTGTCAACAGCCTTGATGACAGGTTTCAAGCTTCAACAGTCTGGT 602
437 GTGTTGAAGATCGAAAGCAGAGTGCACGATTTCTGTCAAGCAACCTTTAGAGCT 496
603 CCATCCGGCCGCAACAGGATACACCGCTCCGTCAACATGCAACCACTTCAATGCTT 662
497 GGGAAACTTAGGATGATGAGGAAATGTATGATGATGATGATGATGATGATGATGAT 556
663 GGAGATCTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 722
557 ATCAAGTAGCGAAGTGTCTAATGATATGATATGATATGATATGATATGATATGATATG 593
723 ACCAGAGGAGTGTGATCTTATCTATGTCACAC 759

```

RESULT 3
AQ160513/c
LOCUS
DEFINITION
  mgxb0006C21r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
  clone mgxb0006C21r, genomic survey sequence.
ACCESSION
  AQ160513
VERSION
  AQ160513.1 GI:3557502
KEYWORDS
  GSS.
SOURCE
  Magnaporthe grisea (anamorph: Pyricularia grisea)
  Magnaporthe grisea
  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
  Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
  1 (bases 1 to 603)
  Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
  Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
  A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
  Genome
  Unpublished
  Contact: Dean RA
  Clemson University Genomics Institute
  100 Jordan Hall, Clemson University, Clemson, SC 29634
  Tel: 864 656 5737
  Fax: 864 656 4293
  Email: rdeane@clemson.edu
  Seq primer: GGAAACAGCTATGACCATG
  Class: BAC ends
  High quality sequence stop: 424.
  Location/Qualifiers
    1..603
      /organism="Magnaporthe grisea"
      /mol_type="genomic DNA"
      /strain="70-15"
      /db_xref="taxon:148305"
      /clone="mgxb0006C21r"
      /tissue_type="Protoplasts"
      /lab_hosts="E. coli DH10B"
      /note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
      Rice blast is one of the most devastating fungal diseases
      of rice world wide. It is a filamentous ascomycete with
      a haploid genome (n=7) of approximately 40 Mbp. Rice
      blast is an important model fungal pathogen for studying
      numerous aspects of the fungal-host interaction. In
      order to facilitate genome wide analysis, a BAC library
      containing 9216 clones with an average insert size of 130
      kbp was constructed. This library represents greater
      than 25x genome coverage. High density colony filters
      are available upon request."
      104 a 152 c 202 g 144 t 1 others
BASE COUNT
  104 a 152 c 202 g 144 t 1 others
ORIGIN
  Query Match 12.5%; Score 82.8; DB 28; Length 603;
  Best Local Similarity 52.8%; Pred. No. 1.9e-08;
  Matches 227; Conservative 0; Mismatches 197; Indels 6; Gaps 2;

QY 154 AAAAAATCAATGAACACCAACACCAAGTTGGTATCATGTCCTCAATCAACTACGGA 213
  |||||
DB 444 AAAAAAAGAGACTACCAACACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 385
  |||||
QY 214 GCCAACTTCCAAACAAATGGTAAATCGGTATTTATGCGTCTATGTTGGACTGTTGACCCCT 273
  |||||
DB 384 GGCAGCTACAGCCCCAGGCAACTCATACCTGGCGGTCTACGGCTGGAGCGGCAACCGC 325
  |||||
QY 274 CTTGTCGATATTATTTGTCAGATGTTGGGCAACTGGCGTCCACCA---GGAGCAACG 330
  |||||
DB 324 CTGATCGAGTACTACGTGGTGAGAGCTTTGGCGAGCTACAAACCCGTCGTGGGCGCCACC 265
  |||||
QY 331 CCTAAGGGGACCATCAGCTGTTGATGGAGGACATATGATATCTACGAGACTCTTAGAGTC 390
  |||||
DB 264 AACCAGGGGCTCTTCACTCGAGCGGACGACCTACGACATCTCTGGTCAGCACCCGGCTAC 205
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```

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QY 391 AATCAACCTCCATTAAAGGGGATTGCCACATTTAAACAATATTGGAGTGTTCGAAGATCG 450
  |||||
DB 204 AACCAGGCTCCATCGACGGCACCAAGACCTTTTCAGCAGTGTCTGGTCGGTCGGCGCAAC 145
  |||||
QY 451 AAACGACGAGTGGCAGCATTTCTGTGAGCAACACTTTAGAGCGTGGGAAACTTAGGG 510
  |||||
DB 144 AAGCGCGCCAGCGGCAACCGTCACCTTTGCCAACCAACGCTCAACGGCTGGCGCAACGCCGCGC 85
  |||||
QY 511 ATGAATATGGGAAATATGTAAGAGTCGCG---CTTACTGTAGAAGGCTATCAAAGTAGC 567
  |||||
DB 84 CTCAACCTCGGCAACCACTGGAATACCAAGATCTCGACCGTCGAGGGCTACCAACAGCAGC 25
  |||||
QY 568 GGAAGTGTCTA 577
  |||||
DB 24 GGCTCCGCCA 15
  |||||

RESULT 4
AQ447125/c
LOCUS
DEFINITION
  mgxb0005C20f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
  clone mgxb0005C20f, genomic survey sequence.
ACCESSION
  AQ447125
VERSION
  AQ447125.1 GI:4576262
KEYWORDS
  GSS.
SOURCE
  Magnaporthe grisea (anamorph: Pyricularia grisea)
  Magnaporthe grisea
  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
  Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
  1 (bases 1 to 670)
  Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
  Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
  A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
  Genome
  Unpublished
  Contact: Dean RA
  Clemson University Genomics Institute
  100 Jordan Hall, Clemson University, Clemson, SC 29634
  Tel: 864 656 5737
  Fax: 864 656 4293
  Email: rdeane@clemson.edu
  Seq primer: TAATCAGCACTCACTATAGGG
  Class: BAC ends
  High quality sequence stop: 263.
  Location/Qualifiers
    1..670
      /organism="Magnaporthe grisea"
      /mol_type="genomic DNA"
      /strain="70-15"
      /db_xref="taxon:148305"
      /clone="mgxb0005C20f"
      /tissue_type="Protoplasts"
      /lab_hosts="E. coli DH10B"
      /note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
      Rice blast is one of the most devastating fungal diseases
      of rice world wide. It is a filamentous ascomycete with
      a haploid genome (n=7) of approximately 40 Mbp. Rice
      blast is an important model fungal pathogen for studying
      numerous aspects of the fungal-host interaction. In
      order to facilitate genome wide analysis, a BAC library
      containing 9216 clones with an average insert size of 130
      kbp was constructed. This library represents greater
      than 25x genome coverage. High density colony filters
      are available upon request."
      114 a 192 c 198 g 166 t
BASE COUNT
  114 a 192 c 198 g 166 t
ORIGIN
  Query Match 12.4%; Score 82.2; DB 28; Length 670;
  Best Local Similarity 54.6%; Pred. No. 2.6e-08;
  Matches 209; Conservative 0; Mismatches 168; Indels 6; Gaps 2;

```

QY 201 CTTAACTGAGAGCCAACTTCCAAACCAATGTATTCGCTATTATTCGCTATTGTTG 260
 DB 397 CATCAACTCTCGGGAGCTTACAGCCCCAGGGCACTATCTGGCCGCTTACGCGCTG 338
 QY 261 GACTGTGACCCCTCTTGTGAAATATATATTTGTGACAGTTGGGGCACTGGCGTCCAC 320
 DB 337 GACGGGCAACCCGCTTATGAGTACTAGCTGTGGAGACTTTGGGACATCAACCCCTG 278
 QY 321 A---GGAGCAACGCCCTTAGGGGACCATCATCTGTTGATGAGAACTATGATCTTACGA 377
 DB 277 GTCCGGCCGCAACCAACCGGGGGGCTTCACTCTGAGCGGACGACATTCAGACATCCTGT 218
 QY 378 GACTCTTAAGTCAATCAACCTTCCATTAAAGGGGATGGCACTTTAAACAATTTGAG 437
 DB 217 CAGCAACCCCTTACMACCACCCTCCATCGACGCGACACGACCTTTACACAGTTCTGTC 158
 QY 438 TGTTCGAAGATGAAAGCAGCAGTGGACAGATTTCTGTACGACCACTTTAGAGCGTG 497
 DB 157 GGTGCGCCGCAACMACCGCGGCCAGCGGACCGTCACTTTGCCACACGTCAACGCGCTG 98
 QY 498 GGAAAACTTAGGATATATATGAGAAATGTATGAAAGTCCG---CTTACTGTAGAACG 554
 DB 97 GGGCAACGCGCGGCTCACTCGGCAACAGTGAATCAAGATCCTGCGCGTCCGAGG 38
 QY 555 CTATCAATAGCGGGAAGTCTTA 577.
 DB 37 CTACCAACAGACGCGCTCCGCCA 15
 RESULT 5
 LOCUS AQ361561 720 bp DNA linear GSS 03-FEB-1999
 DEFINITION mgx00004B19r CUGI Rice Blast BAC library Magnaporthe grisea genomic
 clone mgx00004B19r, genomic survey sequence.
 ACCESSION AQ361561
 VERSION AQ361561.1 GI:4211400
 KEYWORDS GSS.
 SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
 ORGANISM Magnaporthe grisea
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Sordariomycetes Incertae sedis; Magnaporthaceae; Magnaporthe.
 1 (bases 1 to 720)
 Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
 Phillips, K., Sasnowski, M., Wing, R.A. and Dean, R.A.
 A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
 Genome
 JOURNAL Unpublished
 COMMENT Contact: Dean RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson University, Clemson, SC 29634
 Tel: 864 656 5737
 Fax: 864 656 4293
 Email: rdeane@clemson.edu
 Seq primer: GGAAACAGCTATGACCATG
 Class: BAC ends
 High quality sequence stop: 321.
 Location/Qualifiers
 1..720
 /organism="Magnaporthe grisea"
 /mol_type="genomic DNA"
 /db_xref="taxon:148305"
 /db_xref="mgx00004B19r"
 /clone="mgx00004B19r"
 /isolate_type="Protoplasts"
 /lab_host="E. coli DH10B"
 /clone_1lb="CUGI Rice Blast BAC library"
 /note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
 Rice blast is one of the most devastating fungal diseases
 of rice world wide. It is a filamentous ascomycete with
 a haploid genome (n=7) of approximately 40 Mbp. Rice
 blast is an important model fungal pathogen for studying
 numerous aspects of the fungal-host interaction. In

BASE COUNT 137 a 185 c 227 g 170 t 1 others
 ORIGIN
 Query Match 12.4%; Score 82.2; DB 28; Length 720;
 Best Local Similarity 54.1%; Pred. No. 2.6e-08;
 Matches 236; Conservative 0; Mismatches 189; Indels 11; Gaps 3;
 order to facilitate genome wide analysis, a BAC library
 containing 9216 clones with an average insert size of 130
 kbp was constructed. This library represents greater
 than 25x genome coverage. High density colony filters
 are available upon request."
 QY 148 AAAGTAAAAAATTGATGAACACAAACACCAACCAAGTTGGTAATGTCCTTAAC 207
 DB 445 AAAGAAAAAAGAGACTTACACACAAACAAACAAAAA---CAGCGCGCTATCAAC 391
 QY 208 TAGGAGCCAACTTCCAAACCAATATGATGCGTATTATGCGTCTATGAGCTGTT 267
 DB 390 TACTGCGGCGTAAAGCCGCAACGCGGCACTATACCTGCGCTTACGCGTGAACGCGC 331
 QY 268 GACCCCTTTGTCGAATATATATTTGTCGACAGTTGGGCAACTGGCGTCCACA---GGA 324
 DB 330 AACCCGCTGATGAGTACTACGTGAGTGAAGCTTTGGCAGCTACACCCGCTGCGGCG 271
 QY 325 GCAAGCGCTAAGGGGACCATCATCTGTTGATGAGAAATATGATATCTAGACACTCTT 384
 DB 270 GGCACCAACCGCGGCTCTTACCTCGGACGCGACACTTGCAGACATCTGCTGACGACC 211
 QY 385 AGAGTCAATCAACCTCCATTAAAGGATGGGCACTTTAAACAATTTGAGTGTGCA 444
 DB 210 CGCTACAAACACGCTTCATGACGCGCAACAGACCTTTGACGACTTCTGCGGTGCGCC 151
 QY 445 AGATGAAACGACAGTGGCGACGATTTCTGTACGAAACCACTTTAGAGCGTGGAAAAAC 504
 DB 150 CCGCAACAGCGCGCGGCGGCGGCGGCGCTTTCGCAACGTCACAGCGCTCGGCGCAAC 91
 QY 505 TTAGGATGAATATGAGGAAATGTATGAAAGTCCG---CTTACTGTAGAACGCTATCA 561
 DB 90 GCCGCGCTCAACCTTGGGCAACGATGAACTACAGATCTGCGCGCTGAGGCTTACGAC 31
 QY 562 AGTACGGAAGTCTTA 577
 DB 30 AGCAGCGCTCCGCCA 15
 RESULT 6
 LOCUS AQ160254 750 bp DNA linear GSS 09-SEP-1998
 DEFINITION mgx00003L19r CUGI Rice Blast BAC library Magnaporthe grisea genomic
 clone mgx00003L19r, genomic survey sequence.
 ACCESSION AQ160254
 VERSION AQ160254.1 GI:3557243
 KEYWORDS GSS.
 SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
 ORGANISM Magnaporthe grisea
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Sordariomycetes Incertae sedis; Magnaporthaceae; Magnaporthe.
 1 (bases 1 to 750)
 Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
 Phillips, K., Sasnowski, M., Wing, R.A. and Dean, R.A.
 A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
 Genome
 JOURNAL Unpublished
 COMMENT Contact: Dean RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson University, Clemson, SC 29634
 Tel: 864 656 5737
 Fax: 864 656 4293
 Email: rdeane@clemson.edu
 Seq primer: GGAAACAGCTATGACCATG
 Class: BAC ends
 High quality sequence stop: 344.

QY 562 AGTACCGAAGTCTA 577
 DB 85 AGCAGCGGCTCCGCCA 70

RESULT 8
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 LOCUS mgxb0001B24f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
 DEFINITION clone mgxb0001B24f, genomic survey sequence.
 ACCESSION A0399120
 VERSION A0399120.1 GI:4370147
 KEYWORDS GSS.
 SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
 ORGANISM Magnaporthe grisea
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
 1 (bases 1 to 583)
 Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
 Phillips, K., Saslinowski, M., Wing, R.A. and Dean, R.A.
 A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
 Genome
 TITLE Unpublished
 JOURNAL Contact: Dean RA
 COMMENT Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson University, Clemson, SC 29634
 Tel: 864 656 5737
 Fax: 864 656 4293
 Email: rdean@clemson.edu
 Seq primer: TAAATGACTCACTATAGG
 Class: BAC ends
 High quality sequence stop: 411.
 Location/Qualifiers
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 /organism="Magnaporthe grisea"
 /mol_type="genomic DNA"
 /strain="70-15"
 /db_xref="taxon:148305"
 /clone="mgxb0001B24f"
 /tissue_type="Protoplasts"
 /lab_host="E. coli DH10B"
 /clone_1lb="CUGI Rice Blast BAC Library"
 /note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
 Rice blast is one of the most devastating fungal diseases
 of rice world wide. It is a filamentous ascomycete with
 a haploid genome (n=7) of approximately 40 Mbp. Rice
 blast is an important model fungal pathogen for studying
 numerous aspects of the fungal-host interaction. In
 order to facilitate genome wide analysis, a BAC library
 containing 9216 clones with an average insert size of 130
 kbp was constructed. This library represents greater
 than 25x genome coverage. High density colony filters
 are available upon request."

BASE COUNT 104 a 153 c 190 g 136 t
 ORIGIN
 Query Match 12.3%; Score 81.4; DB 28; Length 583;
 Best Local Similarity 52.8%; Pred. No. 3.9e-08;
 Matches 200; Conservative 0; Mismatches 176; Indels 3; Gaps 1;

QY 154 AAAAATTCATGAAACACAAACACCAACCAAGTTGTAACATGTCATTAACATGGA 213
 DB 445 AAGAAAAAAGAGAGACTAATCAACAAACAAACAAAGCGCGCTCACTCACTCG 386
 QY 214 GCCAATTCACCAACAAATGTAATGCTATGCTATGCTGAGCTGTGACCGCT 273
 DB 385 GGCAGCTAAGCCCAAGGCAACTATCTGCGCTGACGCTGAGCGCAACCCG 326
 QY 274 CTTGTCAATATATATGTCGACAGTTGGGCACTGCGCTCAACA--GGAGCAAG 330
 DB 325 CTGATGATCTACTACTGTGTGAGAGCTTTGGCAGCTCAACCCGCTGCGGCGCAC 266

QY 331 CCTAAGGGGACCATCTCTGTTGATGAGAGAAATATGATATCTACAGACTCTTAGATC 390
 DB 265 AACCGGGGCTCTTACCTCGAGCGGACACCTACGACATCTGTGACAGACCGCTAC 206
 QY 391 AATCAACCTCCATTAAGGGGATTGCCACATTTAAACAATATGAGTTCGAAGATCG 450
 DB 205 AACGAGCTCTCATCGACGACCAAGACCTTTGACGAGTTCTGTGCTGCCCGCAAC 146
 QY 451 AAACGACAGTGGCAGCATTTCTGTGACAAACCACTTTAGAGCGTGGGAAACTTAGG 510
 DB 145 AAGCGCGCAGCGGACCGCTCACCCTTCCCAACGCTCAACGCTGCGGACGCGCGC 86
 QY 511 ATGAATATGGGAAATAT 529
 DB 85 CTCACCTCGGCAACCACT 67

RESULT 9
 A0396475/c 561 bp DNA linear GSS 06-MAR-1999
 LOCUS mgxb0010M14f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
 DEFINITION clone mgxb0010M14f, genomic survey sequence.
 ACCESSION A0396475
 VERSION A0396475.1 GI:4367502
 KEYWORDS GSS.
 SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
 ORGANISM Magnaporthe grisea
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
 1 (bases 1 to 561)
 Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
 Phillips, K., Saslinowski, M., Wing, R.A. and Dean, R.A.
 A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
 Genome
 TITLE Unpublished
 JOURNAL Contact: Dean RA
 COMMENT Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson University, Clemson, SC 29634
 Tel: 864 656 5737
 Fax: 864 656 4293
 Email: rdean@clemson.edu
 Seq primer: TAAATGACTCACTATAGG
 Class: BAC ends
 High quality sequence start: 50
 High quality sequence stop: 443.
 Location/Qualifiers
 1..561
 /organism="Magnaporthe grisea"
 /mol_type="genomic DNA"
 /strain="70-15"
 /db_xref="taxon:148305"
 /clone="mgxb0010M14f"
 /tissue_type="Protoplasts"
 /lab_host="E. coli DH10B"
 /clone_1lb="CUGI Rice Blast BAC Library"
 /note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
 Rice blast is one of the most devastating fungal diseases
 of rice world wide. It is a filamentous ascomycete with
 a haploid genome (n=7) of approximately 40 Mbp. Rice
 blast is an important model fungal pathogen for studying
 numerous aspects of the fungal-host interaction. In
 order to facilitate genome wide analysis, a BAC library
 containing 9216 clones with an average insert size of 130
 kbp was constructed. This library represents greater
 than 25x genome coverage. High density colony filters
 are available upon request."

BASE COUNT 99 a 135 c 187 g 137 t 3 others
 ORIGIN
 Query Match 11.6%; Score 76.6; DB 28; Length 561;
 Best Local Similarity 53.7%; Pred. No. 4.7e-07;
 Matches 204; Conservative 0; Mismatches 170; Indels 6; Gaps 2;

QY 139 TTATTCCTTAAGGTAATAAATTCATGAACACAAACACCAACCAAGTTGGTAACATG 198
 |||||
 Db 495 TTTTCCCAAAAGGAAAAAAGAGAGACTANCAAAACACCAACAAACAGCGCGT- 437
 |||||
 QY 199 TCCATAACTACGGAGCCAACTTCCAAACAAATGTAATGCGTATTTATGCGTCTATGGT 258
 |||||
 Db 436 --CATCAACTACTCGGGCAGCTACAGCCCCCGGCAACTCATCTCGCGCTTACGGC 379
 |||||
 QY 259 TGGACTGTGACCCCTCTTGTGCAATATATATATGTCGACAGTTGGGCAACTGGCGTCCA 318
 |||||
 Db 378 TGGAGCGCAACCCGCTGATCGAGTACTACGTGTGGAGAGCTTTGGCAGCTACACCCG 319
 |||||
 QY 319 CCA---GGAGCAACCCCTAAGGGACCACTACTGTGTGATGAGGAACATATGATATCTAC 375
 |||||
 Db 318 TCGTGGCGCGCCACCAACCGCGGCTCTTCACTCGGACGGCAGCACCTACGACATCTCG 259
 |||||
 QY 376 GAGACTCTTAGAGTCAATCAACCTCCATTAAAGGGATGCGACATTTAAACAATATGG 435
 |||||
 Db 258 GTCAGCAGCCGCTACACAGCCCTCCATCGACGCGCACAGACCTTTTCAGAGTTCTGG 199
 |||||
 QY 436 AGTGTTCGAAGATCGAAACGACGAGTGGCGACGATTTCTGTGACGAACCACTTTAGAGCG 495
 |||||
 Db 198 TCGGTGCGCCCAACAGCGCGCAGCGCACCGTCACTTTGCGCAACCACTCAACGCC 139
 |||||
 QY 496 TGGGAAACTTAGGATGAA 515
 |||||
 Db 138 TGGCGCAACGCGCGCTCAA 119
 |||||

RESULT 10
 AQ448084/c
 LOCUS
 DEFINITION mgxb0016B21f CUGi Rice Blast BAC Library Magnaporthe grisea genomic
 clone mgxb0016B21f, genomic survey sequence.
 AQ448084
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Magnaporthe grisea (anamorph: Pyricularia grisea)
 Magnaporthe grisea
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
 1 (bases 1 to 753)
 Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
 Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
 A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
 Genome
 Unpublished
 Contact: Dean RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson University, Clemson, SC 29634
 Tel: 864 656 5737
 Fax: 864 656 4293
 Email: rdean@clemson.edu
 Seq primer: TAATACGACTCACTATAGG
 Class: BAC ends
 High quality sequence stop: 401.
 Location/Qualifiers
 1..753
 /organism="Magnaporthe grisea"
 /mol_type="genomic DNA"
 /strain="70-15"
 /db_xref="taxon:148305"
 /clone="mgxb0016B21f"
 /tissue_type="Protoplasts"
 /lab_host="E. coli DH10B"
 /note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
 Rice blast is one of the most devastating fungal diseases
 of rice world wide. It is a filamentous ascomycete with
 a haploid genome (n=7) of approximately 40 Mbp. Rice
 blast is an important model fungal pathogen for studying

RESULT 11
 AQ398756/c
 LOCUS
 DEFINITION mgxb0005L16f CUGi Rice Blast BAC Library Magnaporthe grisea genomic
 clone mgxb0005L16f, genomic survey sequence.
 AQ398756
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Magnaporthe grisea (anamorph: Pyricularia grisea)
 Magnaporthe grisea
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
 1 (bases 1 to 418)
 Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
 Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
 A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
 Genome
 Unpublished
 Contact: Dean RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson University, Clemson, SC 29634
 Tel: 864 656 5737
 Fax: 864 656 4293
 Email: rdean@clemson.edu
 Seq primer: TAATACGACTCACTATAGG
 Class: BAC ends
 High quality sequence stop: 401.
 Location/Qualifiers
 1..418
 /organism="Magnaporthe grisea"
 /mol_type="genomic DNA"
 /strain="70-15"
 /db_xref="taxon:148305"
 /clone="mgxb0005L16f"
 /tissue_type="Protoplasts"
 /lab_host="E. coli DH10B"
 /note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
 Rice blast is one of the most devastating fungal diseases
 of rice world wide. It is a filamentous ascomycete with
 a haploid genome (n=7) of approximately 40 Mbp. Rice
 blast is an important model fungal pathogen for studying

RESULT 12
 AQ398756
 LOCUS
 DEFINITION mgxb0005L16f CUGi Rice Blast BAC Library Magnaporthe grisea genomic
 clone mgxb0005L16f, genomic survey sequence.
 AQ398756
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Magnaporthe grisea (anamorph: Pyricularia grisea)
 Magnaporthe grisea
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
 1 (bases 1 to 418)
 Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
 Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
 A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
 Genome
 Unpublished
 Contact: Dean RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson University, Clemson, SC 29634
 Tel: 864 656 5737
 Fax: 864 656 4293
 Email: rdean@clemson.edu
 Seq primer: TAATACGACTCACTATAGG
 Class: BAC ends
 High quality sequence stop: 401.
 Location/Qualifiers
 1..418
 /organism="Magnaporthe grisea"
 /mol_type="genomic DNA"
 /strain="70-15"
 /db_xref="taxon:148305"
 /clone="mgxb0005L16f"
 /tissue_type="Protoplasts"
 /lab_host="E. coli DH10B"
 /note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
 Rice blast is one of the most devastating fungal diseases
 of rice world wide. It is a filamentous ascomycete with
 a haploid genome (n=7) of approximately 40 Mbp. Rice
 blast is an important model fungal pathogen for studying

FEATURES
 source
 1..418
 /organism="Magnaporthe grisea"
 /mol_type="genomic DNA"
 /strain="70-15"
 /db_xref="taxon:148305"
 /clone="mgxb0005L16f"
 /tissue_type="Protoplasts"
 /lab_host="E. coli DH10B"
 /note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
 Rice blast is one of the most devastating fungal diseases
 of rice world wide. It is a filamentous ascomycete with
 a haploid genome (n=7) of approximately 40 Mbp. Rice
 blast is an important model fungal pathogen for studying

BASE COUNT 140 a 202 c 253 g 158 t
 ORIGIN
 Query Match 11.3%; Score 74.6; DB 28; Length 753;
 Best Local Similarity 55.1%; Pred. No. 1.4e-06;
 Matches 168; Conservative 0; Mismatches 134; Indels 3; Gaps 1;
 numerous aspects of the fungal-host interaction. In
 order to facilitate genome wide analysis, a BAC library
 containing 9216 clones with an average insert size of 130
 kbp was constructed. This library represents greater
 than 25X genome coverage. High density colony filters
 are available upon request."

QY 201 CATAACTACGAGCCAACTTCCAAACAAATGTAATGCGTATTTATGCGTCTATGGT 260
 |||||
 Db 396 CATCACTACTCGGGCAGCTACAGCCCCCGGCAACTCATCTCGCGCTCTACGGCTG 337
 |||||
 QY 261 GACTGTGACCCCTCTTGTGCAATATATATGTCGACAGTTGGGCAACTGGCGTCCACC 320
 |||||
 Db 336 GACGCGCAACCCGCTGATCGAGTACTAGTGTGGAGAGCTTTGGCAGCTACAACCGCTC 277
 |||||
 QY 321 A---GGAGCAACCGCTTAAGGGGACCATCACTGTTGATGAGGAAACATATATATCTACGA 377
 |||||
 Db 276 GTCGGGCGCCACCATCCGCGGCTCTTCACTCGGACGGCAGCACCTACGACATCTGCT 217
 |||||
 QY 378 GACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATTTGCCACATTTAAACAATATTGGAG 437
 |||||
 Db 216 CAGCACCGCTTACAAACAGCCCTCCATCGAGCGCCCAAGACCTTTTCAGCAGTTCTGCTC 157
 |||||
 QY 438 TGTTCGAAGATCGAAACGACGAGTGGCAGCAATTTCTGTCAGCAACCACTTTAGAGCGTG 497
 |||||
 Db 156 GGTGCGCGCAACAAAGCGCGCCAGCGCACCTTTGCCAACCAACGCTCAACGCGCTG 97
 |||||
 QY 498 GGAAG 502
 |||||
 Db 96 GCAC 92
 |||||

RESULT 11
 AQ398756/c
 LOCUS
 DEFINITION mgxb0005L16f CUGi Rice Blast BAC Library Magnaporthe grisea genomic
 clone mgxb0005L16f, genomic survey sequence.
 AQ398756
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Magnaporthe grisea (anamorph: Pyricularia grisea)
 Magnaporthe grisea
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
 1 (bases 1 to 418)
 Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
 Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
 A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
 Genome
 Unpublished
 Contact: Dean RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson University, Clemson, SC 29634
 Tel: 864 656 5737
 Fax: 864 656 4293
 Email: rdean@clemson.edu
 Seq primer: TAATACGACTCACTATAGG
 Class: BAC ends
 High quality sequence stop: 334.
 Location/Qualifiers
 1..418
 /organism="Magnaporthe grisea"
 /mol_type="genomic DNA"
 /strain="70-15"
 /db_xref="taxon:148305"
 /clone="mgxb0005L16f"

FEATURES
 source
 1..418
 /organism="Magnaporthe grisea"
 /mol_type="genomic DNA"
 /strain="70-15"
 /db_xref="taxon:148305"
 /clone="mgxb0005L16f"

FEATURES
 source
 1..418
 /organism="Magnaporthe grisea"
 /mol_type="genomic DNA"
 /strain="70-15"
 /db_xref="taxon:148305"
 /clone="mgxb0005L16f"

FEATURES
 source
 1..418
 /organism="Magnaporthe grisea"
 /mol_type="genomic DNA"
 /strain="70-15"
 /db_xref="taxon:148305"
 /clone="mgxb0005L16f"


```

REFERENCE 1 (bases 1 to 561)
AUTHORS Zhang,H., Potokina,E., Michalek,W., Weschke,W., Stein,N. and Graner
        A.
TITLE Barley ESTs from germinating seeds
JOURNAL Unpublished
COMMENT Contact: Stein Nils
        Molecular Markers Group, Department Genbank
        Institute of Plant Genetics and Crop Plant Research (IPK)
        Corrensstr. 3, 06466, Gatersleben, Germany
        Tel: 039482-5522
        Fax: 039482-5595
        Email: stein@ipk-gatersleben.de
        Insert Length: 561 Std Error: 0.00
        Plate: 4 row: A column: 2
        Seq primer: M13rev.

FEATURES             Location/Qualifiers
     source           1..561
                     /organism="Hordeum vulgare subsp. vulgare"
                     /mol_type="mRNA"
                     /cultivar="barke"
                     /db_xref="taxon:112509"
                     /clone="HV04A02"
                     /tissue_type="germinating seeds"
                     /dev_stage="germinating seeds (48-96 h)"
                     /lab_host="XL10-Gold"
                     /clone_lib="HV"
                     /note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of
cDNA); Site 2: XhoI (3'-end of cDNA); Roots were grown for
two days on filter paper at room temperature. Due to a
cloning artefact caused by the kit, in most cases the
EcoRI site is NOT present, as well as the EcoRI adapter
used for cloning. To excise the insert, restriction sites
upstream EcoRI should be used (e.g. BamHI, Sali, PstI).
NOTE: Also due to the cloning system used Blue/white
selection for recombinants is not 100% reliable. Average
insert size is 1 kb"
BASE COUNT 117 a 184 c 148 g 112 t
ORIGIN
Query Match          10.0%; Score 66.2; DB 13; Length 561;
Best Local Similarity 57.7%; Pred. No. 0.00011;
Matches 138; Conservative 0; Mismatches 98; Indels 3; Gaps 1;

QY 200 CCAATAACTCGAGCCAACTTCCACCAATGGTAATCGGTATTATTCGGTCTATGGTT 259
DB 320 CGATCAACTCGGCGGATCTTTCCAGCCTCAGGCTACGGTTACCTTCCGGTCTACGGTT 379

QY 260 GGACTGTTGACCTCTTCTCGAATATTATATGTCACAGTTGGGGCACTGGCGTCCAC 319
DB 380 GGACCCGCAACCCGCTTGTGGAGTACTACGTGATCGAGTCTTACGGCACCTTACAACCCCA 439

QY 320 CA---GGAGCAACGCTTAAGGGGACCATCACTGTTGATGGAGGACATATGATATCTACG 376
DB 440 GCAGCGGATCCAGCGCAAGGCGAGCTTCAAGACTGACGGCGGTACCTACGACGTTTCCA 499

QY 377 AGACTCTTAGAGTCAATCAACCTCCATTAAGGGGATGCCACATTTAAACAATATGG 435
DB 500 CCTCACCCGTACCAACCAACGAGCCCTCCATCGATGGAACAAGGACCTTTTCAGCAGTACTGG 558

RESULT 14
LOCUS CD464005
DEFINITION Eth1_48 B06.bl A002 Ethylene-treated seedlings Sorghum bicolor cDNA
clone ETH1_48_B06_A002 3', mRNA sequence.
ACCESSION CD464005
VERSION CD464005.1 GI:31385273
KEYWORDS EST.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.

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REFERENCE 1 (bases 1 to 473)
AUTHORS Cordonnier-Pratt,M.-M., Wentzel,V., Suzuki,Y., Sugano,S., Klein
        R.R., Liang,C., Sun,F., Sullivan,R., Shah,M., Salzman,R., Chua Tan
        N., Gonzalez,M., Lane,S., Miller,V., Nanda,P., Olaseinde,O.,
        Eastman,A. and Pratt,L.H.
TITLE An EST database from Sorghum: 1-aminocyclopropane-1-carboxylic acid
        (ACC)-treated seedlings
JOURNAL Unpublished
COMMENT Other ESTs: ETH1_48 B06.g1 A002
        Contact: Cordonnier-Pratt MM
        Laboratory for Genomics and Bioinformatics
        The University of Georgia, Department of Plant Biology
        Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
        Tel: 706 542 1860
        Fax: 706 583 0210
        Email: mmpratt@uga.edu
        Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
        the Human Genome Center, University of Tokyo Institute of Medical
        Science; plant material and RNA prepared at Texas A & M University;
        sequencing done in the Laboratory for Genomics and Bioinformatics,
        University of Georgia. Sequence ends have been trimmed to exclude
        vector and regions below Phred quality 16. Three-prime sequences
        are presented as their reverse complement and have been trimmed to
        exclude polyA.
        Seq primer: Sug3 (CGACCTGCAGCTCGAGCACA)
        POLYA=Yes.

FEATURES             Location/Qualifiers
     source           1..473
                     /organism="Sorghum bicolor"
                     /mol_type="mRNA"
                     /cultiivar="BTX623"
                     /db_xref="taxon:4558"
                     /clones="ETH1_48 B06 A002"
                     /lab_host="DH10B-T1 phage-resistant E. coli"
                     /clone_lib="Ethylene-treated seedlings"
                     /note="Vector: pME18S-FL3; Site 1: XhoI; Site 2: XhoI; The
library was prepared from polyA+ RNA from seedlings grown
in hydroponic culture. At 8 days of age, medium was
supplemented with 0.5 mM 1-aminocyclopropane-1-carboxylic
acid (ACC) to induce endogenous ethylene (ETH) production.
Roots and shoots were harvested after 27 and 72 hr and
material from both time points was combined prior to RNA
isolation. Double-stranded cDNA was cloned
unidirectionally into different DraIII sites of the
pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG,
3-prime DraIII site is CACCATGTG). XhoI excises the cDNA
insert."
BASE COUNT 109 a 126 c 112 g 126 t
ORIGIN
Query Match          9.5%; Score 63.2; DB 14; Length 473;
Best Local Similarity 53.7%; Pred. No. 0.0005;
Matches 131; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

QY 334 AAGGGGACCATCACTGTTGATGGAGGAACATATGATATCTACGAGACTCTTTAGAGTCAAT 393
DB 16 AAGGGTCAGGTCACTGTTGACGGATCTGTTTACGACATTTACGTACGACCCCGTGTCAAC 75

QY 394 CAACCTCCATTAAGGGGATGCCACATTTAAACAATATTGGAGTGTTCGAAGATCGAAA 453
DB 76 GCCCCTCCATTGAGGGTAACAAGCCCTTTTGGTCTGTTCGACGCAACAAG 135

QY 454 CGCAGCAGTGCACGATTTCTGTGTCAGCAACACACTTTAGAGCGTGGGAAACTTAGGGATG 513
DB 136 CGATCCAGCGGATCCGTCACACCGGTGCTCATTCCAGGCTGGAAATAATGTGGCCCTC 195

QY 514 AATATGGGGAATAATGTTAAGTCCGCTTACTCTAGTAGAGGCTATCAAGTAGCGGAAGT 573
DB 196 ACCCTTGGTAACCAACAATATCAGATCCTTGTCTGTTCAGGGCTACTACAGCTCTGGCTCT 255

QY 574 GCTA 577
DB 256 GCCA 259

```

RESULT 15
BO664593/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

BO664593 483 bp mRNA linear EST 15-JUL-2002
HV04A02u HV Hordeum vulgare subsp. vulgare cDNA clone HV04A02
3-PRIME, mRNA sequence.
BO664593
BO664593.1 GI:21806275
EST.
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Scrophophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Hordeum.
1 (bases 1 to 483)
Zhang, H., Potokina, E., Michalek, W., Weschke, W., Stein, N. and Graner
, A.
Barley ESTs from germinating seeds
Unpublished
Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 483 Std Error: 0.00
Plate: 4 row: A column: 2
Seq primer: M3uni.
Location/Qualifiers
1.483
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Daike"
/db_xref="GABI:148372"
/db_xref="taxon:112509"
/clone="HV04A02"
/issue_type="germinating seeds"
/dev_stage="germinating seeds (48-96 h)"
/lab_host="XLI0-Gold"
/clone_lib="HV"
/note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of
cDNA); Site_2: XhoI (3'-end of cDNA); Roots were grown for
two days on filter paper at room temperature. Due to a
cloning artefact caused by the kit, in most cases the
EcoRI site is NOT present, as well as the EcoRI adapter
used for cloning. To excise the insert, restriction sites
upstream EcoRI should be used (e.g. BamHI, SalI, PstI).
NOTE: Also due to the cloning system used Blue/white
selection for recombinants is not 100% reliable. Average
insert size is 1 kb"

BASE COUNT 102 a 130 c 140 g 111 t
ORIGIN

Query Match 9.1%; Score 60.4; DB 13; Length 483;
Best Local Similarity 51.2%; Pred. No. 0.0021;
Matches 167; Conservative 0; Mismatches 156; Indels 3; Gaps 1;

271 CCTCTTGGAATATATATATGTCAGATGGGCACTGGCGTCC--ACCAGAGCA 327
DB 483 CCGCTTGAGAGTACTGATGATGCTTACGGACCTACACCCGACGAGGATCC 424
QY 328 ACCGCTAAGGGAGCATCTGTTGATGAGAGACATATGATCTACGAGACTTTAGA 387
DB 423 CAGCGGAGGGGAGCTTCAAGACTGACGGGAGTACCTGACCTCCACCCGT 364
QY 388 GTCAATCAACCTCTCAATTAAGGGGATGCCATTTAAACAATATTGAGAGTTCAGA 447
DB 363 ACCAACCACCCCTCCATGATGAGACAGGACCTTCAGCAGTACTGTCTGCCAGC 304
QY 448 TCGAAGCGACAGATGGCAGATTTCTGTACGACACCTTTAGAGGTGGGAAACTTA 507

DB 303 CAGAACCCGTCGAGGAGCAGCTCAACATGCAAAAACCACTTCACGCTGGGCTGTTAC 244
QY 508 GGGATGAATATGGGAAATGTATGAGTCCGCTTACTGTAGAGGCTATCAAGTAGC 567
DB 243 GGCATGAATCTGGGCGACGACTACTACAGATTTGCGCAGTGGGTTTACAGTCTTCT 184
QY 568 GGAAGTCTAATGTATATAGCAATTC 593
DB 183 GGCACCTCGACATCTATGTGCAGAC 158

Search completed: October 20, 2003, 12:03:43
Job time : 2051 secs